Pending Nucleic Acid and/or Pending Amino Acid database searches now generate two sets of results. These databases were split into to two parts to reduce the time needed to update the databases daily. The split freed up more machine time for processing searches.

Searches run against the Nucleic Acid Pending database produce two sets of results, with the extensions, .rnpm and .rnpn
Searches run against the Amino Acid Pending database produce two sets of results, with the

extensions, .rapm and .rapn

The Pending database search results should not be left in the case because they contain data that is confidential.

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/ptodata/2/pna/US6002_COMB.seq:
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have \varepsilon score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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| Description         | Sequence 1, Applis Sequence 2, Applis Sequence 2, Applis Sequence 1059, Applis Sequence 1059, Applis Sequence 149, Applis Sequence 149, Applis Sequence 12166, Applis Sequence 175, Applis Sequence 175, Applis Sequence 175, Applis Sequence 10, Applis Sequence 2311, Applis Sequence 2311, Applis Sequence 1056, Applis Sequence 1056, Applis Sequence 1056, Applis Sequence 156, Applis Sequence 150, Applis Sequence 15 |
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| Score               | 10.25.29.98.89.99.99.99.99.99.99.99.99.99.99.99  |
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|--|---|--|
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| 65 US-60-324-185-25325<br>3 US-07-864-962C-14<br>6 US-08-138-812A-14<br>5 US-08-194-991C-2<br>60 US-60-278-258-10291<br>55 US-60-217-6-754<br>64 US-60-213-175-4<br>64 US-60-131-371-754<br>6 US-08-277-031B-2<br>5 US-08-124-981C-3<br>14 US-09-023-655-1055<br>3 US-07-864-962C-6<br>6 US-08-238-821A-6  | ical<br>ethod<br>R: US/09/763,292<br>0-02-21  | ich  100.0%; Score l'd6; DB 30; Length l  121 Similarity 100.0%; Pred. No. 0;  1746; Conservative 0; Mismatches 0; Indels  cttcaatggatccttttgtggtccttgtgctctctctatgtttgcttctcc  [  |
| 3.2 83.2 183.6<br>6.4 82.3 1893.6<br>6.4 82.3 1893.1<br>1.6 78.6 2880<br>6.6 77.1 1473<br>3.4 76.9 1473<br>3.4 75.9 1473<br>4.6 72.4 2009<br>4.6 72.4 2009<br>4.6 72.4 2009  | pplication US, MATION: B Sangtec Med ENTION: New mc ENTION: New mc ENTION: New mc ENTION NUMBE: 200 to ID NOS: 19 tentin Ver. 2 fertin Ver. 2 | Ouery Match Best Local Similarity 100.0%: Matches 1746; Conservative 0  1 cttcaatggatccttttgtggtcc   |
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| Db 121 TIGGAAATAICCIACAGATAGATATAAGGATGTCAGCAAATCCTTAACCAATCTCICAA 180 | Oy 181 aaatctatggccctgtgttcactctgtattttggcctggaacgcatggtgtgtgctgcatg 240             | Gattgatcttggagaggattttctggaagagcc 30<br>                                   | ya 36<br>   | Oy 361 gatggaagtegattcgcctcatgacgctgcggaatttgggatggga                  | Oy 421 ggagcattgaggaccgtgttcaagaggaagcccgctgccttgtggaggagttgagaaaaa 480  | Oy 481 ccaaggcttcacctgtgatccactttcatcctgggctgtgctcctgcaatgtgatct 540 | Oy 541 gctccattatttccagaaacgtttcgattataaagatcacgaatttcttaacttgatgg 600<br> | Oy 601 aaaaattgaatgaaaacatcaggattgtaagcacccctggatccagatatgcaataatt 660<br>                     | Oy 661 ttcccactatcattgattatttcccgggaacccataacaaattacttaaaaaccttgctt 720   | Oy 721 ttatggaaagtgatattttggagaaagtaaaagaacaccaagaatcgatggacatcaaca 780<br> | Oy 781 acctcgggactttattgattgcttcctgatcaaaatggagaaggaaagccaac 840<br>   | Oy 841 agtctgaattcactattgaaaacttggtaatcactgcagctgacttactt  | Oy 901 cagagacaacacaccctgagatatgctctccttctcctgctgaagcacccagagg 960   11111111111111111111111111111111111 | Oy 961 tcacagctaaagtccaggaagagttgaacgtgtcattggcagaaaccggagccctgca 1020<br> | <ul> <li>Qy 1021 tgcacgacaggggccacatgccctacacagatgctgtggtgcacgaggtccagagataca 1080</li> <li>Dill                                    </li></ul>                    | Oy 1081 tegaceteatececaccagectgececatgeagtgacetgtacgttacatteagacet 1140 | Oy 1141 acetcattcccaagggcacaaccatattaacttccctcacttctgtgctacatgacaaca 1200 | Oy 1201 aagaatttcccaacccagagatgtttgaccctcgtcactttctggatgaaggtggaaatt 1260 |
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| <u> </u>   | 0 10   | o 10   | ි <u>කි</u>   | o 5  | o ∄<br>  | o∵ 1ă  | <u>ت</u> ت   | <br><br>   | O. O.   | O)<br>DE  | O a  | O)   | oy<br>ag   | Qy<br>Db   | Qy<br>Db  | Oy<br>Db  | Oy<br>Op  | ò   |
| 1561   | <pre>Qy 1621 cattaaaaaagtttcactgtgcaaatatatctgctattccccatactctataatagttac 1680</pre> | Oy 1681 attgagtgccacataatgctgatacttgtctaatgttgagttattaacatattatta 1740<br> | Oy 1741 aataga 1746<br>               <br>  Db   1741 aataga 1746 | RESULT 2<br>US-07-864-962C-2<br>; Sequence 2, Application US/07864962C | <ul> <li>GENERAL INFORMATION:         <ul> <li>APPLICANT: Goldstein, Joyce A.</li> <li>APPLICANT: Romkes, Mariorie</li> <li>TITLE OF INVENTION: Cloning and Expression of Complementary</li> </ul> </li> </ul> | DNAs for Multiple Members<br>Subfamily<br>22<br>SS:                  | 60 80  | ; COUNTRY: USA<br>; ZIP: ZOOUS-3918<br>; COMPUTER READABLE FORM:<br>; MEDIUM TYPE: Floppy disk | ; COMPUTER: IBM PC compatible<br>; OPERATING SYSTEM: PC-DOS/MS-DOS<br>; SOFTWARE: Patentin Release #1.0, Version #1.25<br>; CURRENT APPLICATION DATA: | R   | ; NAME: Scott, Walson T.<br>; REGISTRATION NUMBER: 26.581<br>; REFERENCE/DOCKET NUMBER: WTS/5683/92024<br>; TELECOMMUNICATION INFORMATION: | ; TELEPHONE: 202-861-3000<br>; TELERAX: 202-862-0944<br>; TELEX: 6714627 cush<br>; INFORMATION FOR SEQ ID NO: 2: | LD:  | ; TOPOLOGY: linear<br>; MOLECULE TYPE: CDNA<br>US-07-864-962C-2            | Query Match 99.6%; Score 1739.6; DB 3: Length 1746;<br>Best Local Similarity 99.8%; Pred. No. 0;<br>Matches 1742; Conservative 0; Mismatches 4; Indels 0; Gaps 0; | Greetetetetetetetetetetetetetes   | agtga 1   | . e   |

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for 11a of Figure 2."
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0; Mismatches
                                                                                                                                                                                                                         99.6%; Score 1739.6; 99.8%; Pred. No. 0;
       REFERENCE/DOCKET NUMBER: 15280-192-1
            TELECOMMULCATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEPAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1746 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                  Best Local Similarity 99.8 Matches 1742; Conservative
                                                                                                                                                      LOCATION: 1.5
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                         TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                           NAME/KEY: Region
                                                                                                                                                                                        US-08-238-821A-2
                                                                                                                                                                                                                           Query Match
                                                                                                                                FEATURE:
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US-08-238-821A-2
Sequence 2, Application US/08238821A
Sequence 2, Application US/08238821A
Sequence 2, Application US/08238821A
Sequence 3, Application US/08238821A
SERENAL INFORMATION:
APPLICANT: GOLDSTEIN, Joyce A.
APPLICANT: GOLDSTEIN, Joyce A.
TITLE OF INVENTION: CLONING AND EXPRESSION OF COMPLEMENTARY
TITLE OF INVENTION: SUBFAMILY
TITLE OF INVENTION: SUBFAMILY
NUMBER OF SEQUENCES:
COURSESPONDENCE ADDRESS:
COURSESPONDENCE ADDRESS:
COURSESPONDENCE ADDRESS:
                                                                  1201 AAGAATTICCCAACCCAGAGATGTITGACCCTCGTCACTITCTGGATGAAGGTGGAAATT 1260
                     OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/238,821A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION NATA:
APPLICATION NUMBER: US 08/201,118
FILING DATE: 22-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 07/864,962
FILING DATE: 09-APR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Liebeschuetz, Joe
REGISTRATION NUMBER: 37,505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 379 Lytton Avenue CITY: Palo Alto STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                            1741 aataga 1746
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
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REFERENCE/DOCKET NUMBER: PA-0001 US TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/023,655 FILING DATE: HEREWITH
  Sequence 1059, Application US/09023655 GENERAL INFORMATION:
                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1059:
SEQUENCE CHARACTERISTICS:
LENGTH: 1746 base pairs
                                                                                                                                                                                                                                                                                                                                                                       37,071
                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,
                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
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; CLONE: 9181343
US-09-023-655-1059
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                                                                                   960
                                                                                                                                  721 TTATGGAAAGTGATATTTTGGAGAAAGTAAAAGAACACCAAGAATCGATGGACATCAACA
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US-09-023-655-1059
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BLOOD CELL GENE 121 ttggaaatatcctacagatagatattaaggatgtcagcaaatccttaaccaatctctcaa 180 360 Gaps 9 9 attrcccactggctgaaagagctaacagaggatttggaatcgttttcagcaatggaaäga DB 14; Length 1746; 4; Indels OF DETECTION Word Perfect 6.1 for Windows/MS-DOS Ouery Match 99.6%; Score 1739.6; Best Local Similarity 99.8%; Pred. No. 0; Matches 1742; Conservative 0; Mismatches THE APPLICANT COCKS, Benjamin G.
APPLICANT COCKS, Benjamin G.
APPLICANT Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE
TITLE OF INVENTION: EXPRESSION
NUMBER-OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, IN
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA

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| AGA 360         | gaaga 420<br>      <br>GAAGA 420 | aaaaa 480<br>      <br>  <b>Aaaa</b> a 480 | tct 540<br>    <br> CT 540     | tgg 500<br>  | att 550<br>111<br>ATT 560      | ott 720<br>    <br>     720        | 11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 | caac 840<br>  1  <br>CAAC 840 | 99a 900<br>             | 99 960<br>11<br>96 960  | ttgca 1020<br>     <br> TGCA 1020    | taca 1080<br>     <br> TACA 1080 | ct 1140<br>  <br>           | ca 1200<br>          | tt 1260<br>  <br> T 1260           | gg 1320<br>                     | ga 1380<br> }<br>GA 1380          | Eg 1440<br>  -<br> G 1440 |
| TTCAGCAATGGAAA( | ttgggatggg<br>                   | qaggagttgagaa<br>                          | ccctgcaatgtgal<br>             | ttettaaettgate<br>                                   | cagatatgcaataatt<br>           | ttaaaaaccttgc<br>                  | .cgatggacatcaaca<br>                   | gaaaagcaaaacca<br>            | acttggagctg<br>         | ctgaagcaccagagg<br>     | aaaccggagccctg<br>                   | gaggtccagagata<br>               | gttaaattcagaaact<br>        | tgctacatgacaaca<br>  | atgaaggtggaaatt<br>                | tttgtgtgggagag<br>              | gaactttaacct<br>                  | itggatttgcttctc<br>       |
| TTGGAATCGIT     | jacgetgeggaat<br>                | ctgccttgtg<br>                             | atcctgggctgtgct(<br>           | ataaagatcacgaatt<br>           <br> ATAAAGATCAGCAATI | ctggato<br>                    | cataacaaattact<br>                 | aaaagaacaccaagaat<br>                  | itcaaaatggagaagg<br>          | actgcagctgactt<br>      | ctecttetectg<br>        | tcattggcag<br>                       | ctgtggtgcac<br>                  | tgacctgtgac<br>             | teceteaettetgt<br>   | tcacttctgg<br>                     | caggaaaacgga<br>                | cttcattttac<br>                   | octoctattgtcaatg<br>      |
| GAGCTAACAGAGGA  | gttctccctcate<br>                | ttcaagaggaagcccg<br>                       | atcccacttcato                  | aaacgtttcgattat<br>                                  | caggattgtaagcaccc<br>          | tatttccgggaacc<br>                 | ygagaaagt<br>                          | attgetteetgate<br>            | aaaacttggtaatcactgc<br> | icaaccetgagatatgeti<br> | aagagattgaacgtg<br>                  | gecetacacagatg<br>               | cctgccccatgcag<br>          | ggcaccatattaactt<br> | gatgtttgaccetes<br>                | catgcctttctcago                 | gttttattcctgad<br>                | ggaccttgacacaa<br>        |
| CCACTGGCTGAAA   | aaggagattegge<br>                | cattgaggaccgtg <br>                        | gcttcaccctgtg<br>              | attatttccag<br>                                      | ttgaatgaaaacatc<br>            | tatcattgat<br>                     | gaaagtgatatttc<br>                     | cgggactttattga<br>            | gaattcactattga<br>      | caacaagce<br>           | ctaaagtccagg<br>                     | acaggggccacatgd<br>              | ctcatccccaccago<br>         | CCCAAGO              | tcccaacccaga<br>                   | aaaagtaactactt<br>              | ccgcatggagct<br>                  | tgattgacccaaa<br>         |
| 01 ATTIC        | 61 gatgg<br>      <br>61 GATGG   | 21 ggag<br>         <br>21 GGAG            | 81 ccaag<br>      <br>81 CCAAG | 41 gctcc<br>        <br>41 GCTCC                     | 01 aaaaa<br>      <br>01 AAAAA | 61 ttcccac<br>          61 TTCCCAC | 21 ttatge<br>       <br>21 TTATG       | 81 accete<br>                 | 41 AGTCTG               | 01 cagagad<br>          | 961 tcacag<br>        <br>961 TCACAG | 1 tgcacg<br>                     | 1 tcgac<br>11111<br>1 TCGAC | 1 acctcatt           | l aagaat<br>          <br>  AAGAAT | 1 ttaag<br>        <br>   TTAAG | 1 gcctgg<br>         <br>  GCCTGG | 1 aatoto<br>              |
| Db 3            | Oy 3<br>Db 3                     | 0y 4<br>Db 4                               | Qy 4<br>Db 4                   | 0y 5<br>Db 5   | 0y 6<br>Db 6                   | Oy 6                               | Oy 7:                                  | 0y 71<br>15 da                | Oy 8,                   | Oy 90                   | Oy 96:                               | Oy 102:                          | Oy 108<br>Db 108            | Oy 114<br>Db 114     | Oy 120                             | Oy 126<br>Db 126                | Oy 132<br>Db 132                  | Oy 138<br>Db 138          |

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    51 tctggagacagagctctgggagagagaaactcctcctggccccactcctcccagtga 120
    51 tctggagacagagctctgggagagagaaactccctcctgggcccactcctcccagtga 120
    51 tctggagacagagctctgggagagaaaactccctcctggcccactcctcccagtga 120

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 99.6%; Score 1739.6; DB 31; Length 1746; Best Local Similarity 99.8%; Pred. No. 0; Matches 1742; Conservative 0; Mismatches 4; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: HOINE, Darci T.

APPLICANT: Wockley, Joseph G.
APPLICANT: Scherf, Uwe
APPLICANT: Gene Logic, Inc.
APPLICANT: Gene Logic, Inc.
TILLE OF INVENTION: Gene Expression Profiles in Liver Cancer
FILE REFERENCE: 44921-5028-W0
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR PRILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Genbank Accession No. M61854 US-09-880-107-2370
                                                                                                                                                                                                                                                                                                                                                                          : Sequence 2370, Application US/09880107 : GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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US-09-880-107-2370
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: SOFTWARE: Pater
: SEQ ID NO 2370
: LENGTH: 1746
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APPLICANT: Malsen, Gareth
APPLICANT: Townley, David
APPLICANT: Townley, David
APPLICANT: Fownley, David
APPLICANT: MacDonald
TILE OF INVENTION: Single Nucleotide Polymorphisms Associated With ADME Genes
FILE REFERENCE: GX-0013-1 P
CURRENT APPLICATION NUMBER: US/60/226,176
CURRENT FILING DAIE: 2000-08-16
NUMBER OF SEO ID NOS: 2447
SEO ID NO 749
LENGTH: 1746
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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99.6%; Score 1739.6;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1742; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                     US-60-226-176-749
: Sequence 749, Application US/60226176
: GENERAL INFORMATION:
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OTHER INFORMATION: GB:HUMCYPC219
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|--|---|---|---|--|--|--|---|--|--|---|---|--|---|--|--|---|---|
|  | tgaaagagctaacagagatttggaatcgttttcagcaatggaaaga<br>                        | gogtttotcoctcatgacgotgoggaattttgggatggga                                      | ccttgtggaggagttgagaaaaa 4<br>   | 2y 481 ccaaggetteacectgtgateceaettteateetgggetgtgeteeetggaatgtgatet 540      | Oy 541 getecattattitecagaaacgiticgattataaagateacgaatticitaactigaigg 600<br>  | Oy 601 aaaaattgaatgaaaacatcaggattgtaagcacccctggatccagatatgcaataatt 560<br>     | Oy 661 ttcccactatcattgattatttcccgggaacccataacaaattacttaaaaaccttgctt 720<br> | Oy 721 ttatggaaagtgatattttggagaaagtaaaagaacaccaagaatcgatgacatcaaca 780<br> | Cy 781 accetegggaetttattgattgetteetgateaaatggagaaaggaaaageaaaecaae 840<br> | Oy 841 agtotgaattoactattgaaaacttggtaatoactgooggtgacttacttggagotggga 900<br>   | Oy 901 cagagacaacaagcacaaccctgagatatgctctcttctcctgctgaagcaccagagg 960<br>   | Oy 961 tcacagctaaagtccaggaagagttgaacgtgtcattggcagaaaccggagccctgca 1020<br> | Oy 1021 tgcacgacaggggccacatgccctacacagatgctgtggtgcacgaggtccagagataca 1080<br>       | <pre>// 1081 tegaceteateceaccageetgeceatgeagtgacetgtgacgttaaatteagaaact 1140  </pre> | Oy 1141 acctcattcccaagggcacaaccatttaacttccctcacttctgtgctacatgacaaca 1200<br>       | Oy 1201 aagaatttoocaacocagatgtttgacoctogtoactttotggatgaaggtggaaatt 1250<br> | . Oy 1261 ttaagaaaagtaactactcatgccttctcagcagaaaacgaattgtgtgggagagg 1320<br>   |

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| 1201      | 1261  | 1261             | 1321             | 1381       | 1381                             | 1441    | 1441                    | 1501   | 1501                                    | 1561   | 1561          | 1621  | 1521            | 1681             | 1681  | 1741        | 1741   | F       | 0-313                  | NEPAL<br>PPL IC | APPLIC!<br>APPLIC! | PPLICA   | ILE RE           | URRENT | SOFTWAR<br>EQ ID N | LENGTH<br>TYPE: | ORGANI                                   | NAME/I | 0-313        | ery Ma |                           | 1  | 1     | 51   |
|-----------|-------|------------------|------------------|------------|----------------------------------|---------|-------------------------|--------|---|--------|---------------|-------|-----------------|------------------|---|-------------|--|---------|------------------------|-----------------|--------------------|----------|------------------|--------|--------------------|-----------------|--|--------|--------------|--------|---------------------------|--|-------|--|
| QQ        | Οy    | Op               | Oy<br>Dp         | č          | 64<br>0p                         | oy      | qq                      | Οy     | qq                                      | 0y     | qq            | Оу    | οp              | Qy               | qq.   | O.          | q  | 1500    |                        |                 |                    |          |                  |        |                    |                 |  |        | 9-Sn         | õ      | Ma                        | Oy   | Dp    | Οÿ   |
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| ggatg     | tttt  |                  | gccctgattgatcttg | tgato      | ctggctgaaagagctaacagaggatttg<br> | 4999    |                         |        |   | cated  | HIII          | ttata | HIII            | aadca            | 1111  | 6           | 3accc<br>    <del> </del>      <br>3accc           | 38880   | 1111                   | yatca           | <br>gatca          | atca     | HII!             | gete   | <br> gctc          | cgtg            | IIII<br>Icgtg                            | ıgatg  |              | m.     | - m                       | actt   | actt  | cctc   |
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| <br>agata | Sacto | Jacto            | 3gccc            | 39000      | ageta<br>                        | 10.4    | ttot                    | מ      |   | CCCa   |               | cgtt  | IIII<br>Icgtt   | agga             | 1111  |             | 11 = 1   | qaqa    | i i i i i              | tgct            | IIII<br>tgct       | aact     | aact             | ctga   | ctga               | gaga            | gaga                                     | accti  | cccti        | ctgc   | ctgc                      | acca   | acca  | aaitteceaaceayagatgtttgaecetegteaettetggatgaaggt |
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| Hill      | tggc  |                  | agtggt<br>       | lagtg      | actg                             |         | n — 10                  | 1000   | 1111<br>1111                            | ttca   | HIII          | tatt  | <br> tatt       | gaat             | inni<br>qaat  | ,           | Late   | aagt    | _ ë                    | ggac            | <br>ggac           | attc     | atto             | aaca   | aaca               | taaa            | taaa                                     | cagg   | _ Si _       | catc   | cato                      | tece   | tccc  | tccci  |
|           | atcta |                  | gatatgaag        | rarge      | itttcccac                        | למם לי  | gatggaagg               | agnat  | ggagcattgagg                            | aaggo  |               | tccat |                 | aaatt            | aaaaattaaataaaacatcaagattataaacacccctaaatcaataataca |             |  | atgga   |                        | scteg           |                    | tctga    |                  | jagac  |                    | cage            | tcacagctaaagtccaggaagagattgaacgtgtcattgg | sacga  | III III      | jacct  | tcgacct                   | cctcattcccaagggcacaaccatattaacttccctcacttctgtg | tcat  | gaatt  |
|           | _     |                  |                  |            | 10 - 10                          | , ,     |                         | _      |   | _      |               | -     | <u>—</u> თ      |                  |   |             |  | 7       |                        | 1<br>a          | – ¤                | ь.<br>Б. |                  | S.     | _ B                |                 |  |        | Ξħ,          |        |                           | ø -  | - rū  | a<br>  |
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|           |       |                  |                  | "          |                                  |         | ٠.                      |        |   |        |               |       |                 |                  |   |             |  |         |                        |                 |                    |          |                  |        |                    |                 |  |        |              |        |                           |  |       |  |

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R INFORMATION: GB:HUMCYPC219
3-371-749
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Sequence 58, Application US/09488127 GENERAL INFORMATION:
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Best Local Similarity
Matches 1742; Conserv
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; ORGANISM: HOMO
US-09-488-127-58
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1740 60 Gaps aagaatttoccaacoccaqaqatgtttgacoctcgtcactttotggatgaaggtggaaatt Length 1748; .. 4; Indels STRUCTURE 18; DB GENE Score 1739.6; Pred. No. 0; 0; Mismatches APPLICANT: Thomann, Hans-Ulrich
APPLICANT: Thomann, Hans-Ulrich
TITLE OF INVENTION: RAPID DETERMINATION OF
TITLE OF INVENTION: USING CDNA SEQUENCE
FILE REFERENCE: 2709.1005-000
CURRENT APPLICATION NUMBER: US/09/488.127
CURRENT FILING DATE: 2000-01-20
NUMBER OF SEQ ID NOS: 96
SOFTWARE: FastSEQ for Windows Version 4.0 OF

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| Oy 1201 aagaatttcccaacccagagatgttgaccalling of 1203 aagaattcccaacccagagatgttgaccoord 1203 aagaattcccaacccagagatgttgaccoord 1203 ttaagaaaagtaactacttcatgccttctctcll 1111111111111111111111111111 | Oy 1381 aatctctgattgacccaaaggaccttgacae | 0y 1561 tettetgaccegteateteacattttecett Db 1563 tettetgaccegteateteacattttecett Oy 1621 cattaaaaagttteactgtgcaaatatate | Db 1683 attgagtgccacataatgctgatacttgtct | GENOLI 1278-58 Sequence 58, Application US/09488127B GENERAL INFORMATION: APPLICANT: Thomann, Hans-Ulrich TITLE OF INVENTION: RAPID DETERMINATION: TITLE OF INVENTION: RAPID DETERMINATION: FILE REFERENCE: 2709.1005-000 CURRENT APPLICATION NUMBER: US/09488, CURRENT APPLICATION NUMBER: US/09488 | : NUMBER OF SEQ ID NOS: 97 : SOFTWARE: FastSEQ for Windows Version : SEQ ID NO 58 : LENGTH: 1748 : TYPE: DNA : ORGANISM: HOMO Sapiens US-09-488-127B-58 | Ouery Match Best Local Similarity 99.6%; Score I: Best Local Similarity 99.8%; Pred. Nammatches 1742; Conservative 0; Mismm 0y 1 cttcaatggatccttttgtggtccttgtgctc |
|---|---|--|---|--|---|---|
| 121 tiggaaatatcctacagatagatattaaggatgicagcaaatccttaaccaatctctcaa 180  |   | itcaccctgtgatcccacttcatcctgggctgqctccctgcaatgatc; 54   |   | 78<br>84<br>84<br>90<br>90   | 1 cagagacaacaagcacaa<br>  | 1023 tgaagadagagacaatgacctacacagatgctgtggtgcagaggtccagagataca 1080   11   |
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| ttggaaatatoctacagatagatattaaggatgtoagcaaatocttaacoaatototoa<br> | aaatctatggccctgtgttcactctgtattttggcctggaacgcatggtggtgtcgcatg<br> | ggaag<br>           <br>ggaag | gaatcgttttcagcaatggaag | atggaaggattcgcgtttctcctcatgacggaatcgtttcagcaatggaaag<br>hllllllllllllllllllllllllllllllll | gagcattgaggaccgtgttcaagaggaagccgctgccttgtggaggaagtgaggaag<br> | ccactttcatcctgggctgtgctcctgcaatgtgatc | gctccattatttccagaaacgittcgattataaagatcacgaattcttaacttgatgg<br> |          | ttcccactatcattgattatttcccgggaacccataacaaattacttaaaaaccttgctt<br> | ttatggaaagtgatattttggagaaagtaaaggaacaccaagaatcgatggacatcaaca<br> | accttoggactttattgattgcttcttgatcaaatggagaaggaaagcaaaccaac<br> | agtctgaattcactattgaaaacttggtaatcactgcagctgacttactt | cagagacaacaagcacaaccctgagatatgctctccttctctgctgagagcacccagagg<br> | tcacagctaaagtccaggaagagattgaacgtgtcattggcagaaaccggagccctgca<br> | tgcacgacaggggccacatgccctacacagatgctgtggtgcacgaggtccagagataca<br> | togacctcatccccaccagcctgcccatgcagtgacctgtgacgttaaattcagaaact<br> | acctcattcccaagggcacaaccatattaacttccctcacttctgtgctacatgacaaca<br> | aagaatttcccaacccagagatgtttgaccctcgtcactttctggatgaaggtggaaatt |
| 121   | 181  | 241                           | 301                    | وت نوت  | 2 2   | 481                                   | 541  | 601      | 661<br>663   | 721  | 781  | 841  | 901  | 196   | 1021   | 1081  | 1141   | 1201   |
| Oy<br>Op  | Oy<br>Dp   | Oy<br>Op                      | oy<br>Db               | Oy<br>Db  | Oy<br>Dp  | Oy<br>Dp                              | Oy<br>Db   | Oy<br>Op | Oy<br>Dp   | Oy<br>Dp   | Qy<br>Dp   | Oy<br>Db   | Oy<br>Db   | Qy<br>Dp  | Qy<br>Db   | Oy<br>Db  | Qy<br>Dp   | ον   |

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DB 27; Length 1940;
                                                                                                                                                                                                                                                                                                                                               Sequence 12366, Application US/09698010

GENERAL INFORMATION:
APPLICANT: Williamson, Mark
APPLICANT: Shyjan, Andrew W.
ITILE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
ITILE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
FILE REFERENCE: 1600. 2029-001

CURRENT FILING DATE: 2000-10-27

PRIOR PILING DATE: 1999-10-29

PRIOR FILING DATE: 1999-10-29

NUMBER OF SEQ ID NOS: 15684

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93.1%; Score 1625.2;
96.3%; Pred. No. 0;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LCCATION: (1)...(1940)
: OTHER INFORMATION: n = A/T,C or G
US-09-698-010-12366
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Best Local Similarity 96.33
Matches 1691; Conservative
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ORGANISM: Homo sapiens
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| ###################################### | cctacagatagatattitaggatgtcagcaaatccttaaccaatctccaaaatcta<br>ccctgtgttcactctgtattttggcctggaacgcatgatggtgctgcatggataga<br> | Lggtgaaggaagcctgattgatcttggagagggttttctggaagaggccatttccc 3<br> | tggctgaaagagctaacagagatttggaatcgtttcagcaatggaaagagatggaa 3<br> | agatteggegttteteeetealgaegetgeggaattteggaalggggaaggggeet 4<br> | aagaccgigitcaagaggaagcccgctgcctcgigaagagtigagaaaaaccaaggc 4<br> | cacctgtgatcccactttcatcctgggctgtgctccctgcaatgtgatctgctccat | ttttccagaaacgittcgattataaagatcacgaattcttaacttgatggaaaaati (<br> | atgaaaacatcaggattgtaagcacccctggatccagatatgcaataatttcccac (<br> | tcattgattatttcccgggaacccataacaaattacttaaaaaccttgcttttatgga<br> | gtgatattttggagaaagtaaaggacaccaagaatcgatgacatcaacaaccetcg<br> | actttatigatigcticcigatcaaaaiggagaaggaaaagcaaaaccaacagiciga (<br> | tcactattgaaaacttggtaatcactgcagctgacttactt | caagcacaaccctgagatatgctctccttctcctgctgaagcacccagaggtcacagc | aaagtccaggaagagattgaacgtgtcattggcagaaaccggagccctgcatgca | aggggccacatgccctacacagatgctgtggtgcacgaggtccagagatacatcgacct<br> | atccccaccagcctgccccatgcagtgacctgtgacgttaaattcagaaactacctcat<br> |
| 61 ac<br>128 ta                        | 121 ta<br>188 tg<br>11<br>181 tg   | 248 ag<br>   <br>241 ag  | 308 ac<br>  <br>  108  | 368 99<br>  <br>361 99   | 428 tg<br>  <br> 421 tg   | 488 tt<br>  <br> 481 tt                                   | 548 ta<br>  <br>541 ta  | 608 ga<br>  <br>601 ga   | 668 ta<br>  <br>661 ta   | 728 aa<br>  <br> 721 aa                                      | 788 99<br>  <br>781 99   | 848 at                                    | 908 aa<br>  <br>901 aa                                     | 968 të<br>1<br>961 të                                   | 1028 Cd   | 1088 c  |
| oy<br>Oy                               | Oy<br>Oy<br>Ob   | Oy<br>Dp   | Oy<br>Db   | Oy<br>Db   | Oy<br>Dp  | Oy<br>Dp  | Qy<br>Db  | Oy<br>Db   | Oy<br>Db   | Oy<br>Db   | Oy<br>Dp   | Oy<br>Db                                  | Oy<br>Db   | Qy  | Qy<br>Db  | Qy<br>Db  |

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IIILE OF INVENTION: FUNCTIONAL BACTERIAL/MAMMALIAN CYTOCHROME P450 CHIMERA
FILE REFERENCE: 176/60232
CURRENT PAPLICATION NUMBER: PCT/US98/16979
CURRENT FILING DATE: 1998-08-17
EARLIER APPLICATION NUMBER: 60/056,754
EARLIER FILING DATE: 1997-08-20
SUMMER OF EQ. ID NOS: 14
SOFTWARE: PATENTIN Ver. 2.0
                                                                                                                                                  1447
1381 ggttgacccaaaqaaccttgacaccactccagttgtcaatggatttgcctctgtgccgcc 1440
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Pred. No. 0;
0; Mismatches
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Best Local Similarity 92.9%;
Matches 1637; Conservative (
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TYPE: DNA
ORGANISM: mammalian
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PCT-US98-16979-4
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|--|--|-------------------------------------|---------------------------------------|--------------------------------------|-----------------------------------|------------------------------------|--------------------------------------|--------------------------------------|--------------------------------------|---------------------------------------|--|-------------------------------------|--------------------------------------|--------------------------------------|--------------------------------------|--|--------------------------------------|----------------------------------|
| 1 tctggagacagagctctgggagagagagaaact.<br> | agatattaagga<br>            <br>aggtattaagga | atctatggccctgtgttcactctgtattt<br>   | 1 gatatgaagtggtgaaggaagccctgattga<br> | 1 atttcccactggctgaaaga<br>           | gatggaaggagattcggcgtttctccctc<br> | ggagcattgaggaccgtgttcaagaggaag<br> | 1 ccaaggettcaccetgtgateceaetttea<br> | 1 gctccattattttccagaaacgtttcgatt<br> | l aaaaattgaatgaaaacatcaggattgtaa<br> | 1 ttcccactatcattgattatttcccgggaa<br>  | l ttatggaaagigatatttiggagaaagtaa.<br>  | 1 acctcgggactttattgattgcttcctga<br> | 1 agtctgaattcactattgaaaacttggtaa<br> | 1 cagagacaacaagcacaaccctgagatatg<br> | 1 tcacagctaaagtccaggaagagattgaac<br> | 1 tgcacgacaggggccacatgccctacacag<br>   | gacctcatccccaccagcctgcccatg          | 1 acctcattcccaaqqqcacaaccatattaa |
| 61                                       | 121  |                                     |                                       | 301                                  | 36.                               | 42.                                | 48                                   |                                      | 09                                   | 99                                    | 72                                     |                                     | 84                                   | 06                                   | 96                                   | 102                                    | 108                                  |                                  |
| oy<br>Db                                 | oy<br>Db                                     | oy<br>Dp                            | 9.<br>9.                              | Oy.                                  | Oy<br>Dp                          | Oy<br>Db                           | oy<br>Dp                             | Oy<br>Dp                             | oy<br>ob                             | 9.y<br>0.b                            | Oy<br>Db                               | Oy<br>Dp                            | 9                                    | Oy<br>Dp                             | Oy<br>Db                             | Oy<br>Db                               | oy a                                 | 6 6                              |

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RESULT 13
US-09-023-655-1057
Squence 1057, Application US/09023655
GENERAL INFORMATION:
APPLICANT: Gocks, Benjamin G.
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
STREET: 3174 PORTER DRIVE
COUNTRY: USA
                                                                                          1441 tecegecettetateagetgtgetteatteetgtetgaagaageaeagatggtetggetg 1500\,
                                                                                                                                                                       1554 tgatgettettetgaccegleateteacatttecetteececaagatetagtgaacatt 1513
                                                                                                                                                                                                                                                  ZIP: 94304

ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                    Score 1534.6;
Pred. No. 0;
0; Mismatches
CLASSIFICATION:

**ATORNEY_AGENT INFORMATION:
**NAME: Zeller, Karen J.
**RECISTRATION NUMBER: 37,071
**REFERENCE/DOCKET NUMBER: PA-0001 US
**TELECOMMUNICATION INFORMATION:
**TELEPHONE: (650) 845-0555
**TELEFAX: (650) 845-4166
**INFORMATION FOR SEQ ID NO: 1057:
**SEQUENCE CHARACTERISTICS:
**LENGTH: 1845 base pairs
**TYPE: nucleic acid
**STRANDENESS: single
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CLONE: 9181302
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Sequence 4, Application US/09135296
GENERAL INFORMATION:
APPLICANT: Jones, Jeffrey P.
APPLICANT: Shimoji, Miyuki
TITLE OF INVENTION: FUNCTIONAL BACTERIAL/MAMMALIAN CYTOCHROME P450 (CURENT APPLICATION NUMBER: US/09/135,296
CURRENT APPLICATION NUMBER: US/09/135,296
CURRENT APPLICATION NUMBER: 60/056,754
EARLIER FILING DATE: 1997-08-20
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
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Pred. No. 0;
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ilarity 92.9%;
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: ORGANISM: manmalian
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Pred. No. 0;
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               APPLICANT: Malsen, Gareth
APPLICANT: Malsen, Gareth
APPLICANT: Townley, David
APPLICANT: Townley, David
TILLE OF INVENTION: Single Nucleotide Polyme
FILE REPERENCE: GX-0013-1P
CURRENT APPLICATION NUMBER: US/60/226,176
UNUMBER OF SEQ ID NOS: 2447
SEQ ID NO 753
   Sequence 753, Application US/60226176 GENERAL INFORMATION:
                                                                                                                  NAME/KEY: misc_feature
OTHER INFORMATION: GB:HUMCYP2C9A
-60-226-176-753
                                                                                                                                                     87.9%;
92.9%;
                                                                                                                                                            st Local Similarity 92.9 tches 1637; Conservative
                                                                                                       sapiens
                                                                                                TYPE: DNA
ORGANISM: HOMO
                                                                                         LENGTH: 1845
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Search completed: April 19, 2002, 11:02:26 Job time: 13246 sec

429, APP 429, APP 429, APP 429, APP 429, APP 429, APP 2353, APP 12135, A 12432, A 10573, A 10073, APP

Sequence Sequence A Sequence A Sequence A Sequence A Sequence A Sequence B Se

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10538 AGGAATCITGITITCIAACCGGCCGTGCTGGTGGACACTGCGCAATTTTGCACTTGGAGC 10479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Rosen, et. al
TILE OF INVENTION: Human Secreted Proteins
FILE REFERENCE: PS950
CURRENT PPLICATION NUMBER: US/10/105,299
CURRENT FILING DATE: 2002-03-26
NUMBER OF SEQ ID NOS: 15197
Prior Application removed · See File Wrapper or Palm
SSOFWARE: Patentin Ver. 2.0
SEQ ID NO 7201
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US-09-978-681A-429
US-09-978-564-429
US-09-999-831A-429
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US-10-013-921A-429
US-10-013-921A-429
US-10-013-921A-429
US-10-013-929A-429
US-10-013-929-2363
US-10-105-299-1235
US-10-105-299-12435
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US-10-105-299-12435
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US-10-105-299-6773
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: Sequence 12104, Application US/10105299
: GENERAL INFORMATION:
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; Sequence 7201, Appliqation US/10105299
; GENERAL INFORMATION:
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Best Local Similarity 53.9
Matches 83: Conservative
    ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-105-299-7201
    000000000000000000000
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Sequence 1204, A
Sequence 100, App
Sequence 12117, A
Sequence 12117, A
Sequence 1217, A
Sequence 140, App
Sequence 21327, A
Sequence 21327, A
Sequence 2 3227, A
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376.816 Million cell updates/sec
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1604, Ap
7023, Ap
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                                                                                                                                                                  April 19, 2002, 11:06:02 ; Search time 232.27 Seconds
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(gan2_6/ptodata/2/pna/USO5_NEW_COMB.seq:*

(gan2_6/ptodata/2/pna/USO5_NEW_COMB.seq:*):

(gan2_6/ptodata/2/pna/USO3_NEW_COMB.seq:*):

(gan2_6/ptodata/2/pna/USO9_NEW_COMB.seq:*):

(gan2_6/ptodata/2/pna/USO9_NEW_COMB.seq:*):

(gan2_6/ptodata/2/pna/USO9_NEW_COMB.seq:*):

(gan2_6/ptodata/2/pna/USO9_NEW_COMB.seq:*):
                             GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-10-105-299-12104
US-10-103-213-1207
US-10-105-299-12317
US-10-105-299-11317
US-10-105-299-11849
US-10-105-299-11849
US-10-105-299-1237
US-10-105-299-1203
US-10-105-299-1203
US-10-105-299-1203
US-10-105-299-1203
US-10-105-299-1203
US-10-105-299-1203
US-10-105-299-1203
US-10-105-299-14391
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DB seq length: 2000000000
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NUMBER OF SEQ ID NOS: 31255
SEQ ID NO 20507
LENGIH: 266
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICAN: SYLUM: Joseph R.
APPLICAN: Byrum: Joseph R.
APPLICAN: La Rosa, Thomas J.
ITIE DE INVENTION: Nucleic Acid Molecules and Other Molec: es Associated With ITILE OF INVENTION: Plants
FILE REFERENCE: 38-21(15309)8
FILE REFERENCE: 38-21(15309)8
CURRENT APPLICATION WINGER: US/09/975,254
CURRENT FILING DAIE: 2001-10-12
PRIOR FILING DAIE: 1999-03-05
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                                                                                                       Ouery Match
4.7%: Score 35; DB 5; Length 111:5;
Best Local Similarity 55.3%; Pred. No. 1.2;
Matches 68: Conservative 0; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Rosen et al.
TILE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PJ20071
CURRENT APPLICATION NUMBER: US/10/103,313
CURRENT FILING DAIE: 2002-03-12
NUMBER OF SEO ID NOS: 553
Prior Application removed · See File Wrapper or Palm
SOFTWARE: Patentin Ver. 2.0
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               : TYPE: DNA
: ORGANISM: Homo sapiens
US-10-105-299-12104
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Best Local Similarity
Matches 75; Conserv
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LENGTH: 11146
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:S-10-103-313-100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                157 ctctctctcaagtagccaaagtacttacttgaaaatggtcaagtcctttctagca 216
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                                                                                                                                                     Length 266;
                                                                                                                                                                                            90; Indels
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CURRENT APPLICATION NUMBER: US/10/105,299
CURRENT FILING DAIE: 2002-03-26
NUMBER QE_SEQ ID NOS: 15197
Prior Application removed - See File Wrapper or Palm SCFINARE: Datentin Ver. 2.0
SEG ID NO 12317
LENGTH: 52845
                                                                                                                                        Ouery Match
Best Local Similarity 51.6%; Pred. No. 0.41;
Matches 97; Conservative 0: Mismatches 90;
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Pred. No. 9.1;
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TYPE: DNA
ORGANISM: Glycine max
OTHER INFORMATION: Clone ID: 700958447H1
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Sequence 12317, Application US/10105299
SENEFAL INFORMATION:
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..s-10-105-299-11849/c
. Sequence 11849. Application US/10105299
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Best Local Similarity 48.4%;
Matches 92: Conservative
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: ORGANISM: Homo sapiens
#S-10-105-299.12317
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                                                                      US-09-975-254-20507
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APPLICANT: Byrum, Joseph R.
APPLICANT: Byrum, Joseph R.
APPLICANT: Brow, Gregory R.
APPLICANT: La Rosa, Thomas J.
IILE CF INVENTION: Uncleic Acid Molecules and Other Molecules Associated With
IILE CF INVENTION: Plants
FILE REFERENCE: 38-21(15309)8
FURERIY PRILING DATE: 2001-10-12
FRICR APPLICATION NUMBER: US/09/263,191
FRICR APPLICATION NUMBER: US/09/263,191
NUMBER OF SEQ ID NOS: 31255
SEQ ID NO 24327
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4.3%; Score 32.2; DB 5; Length 261:
Best Local Similarity 57.4%; Pred. No. 1.2;
Matches 58; Conservative 0; Mismatches 43; Indels
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GENERAL INFORMATION:
APPLICANT: Barnes, John T.
APPLICANT: Bertin, John
IIILE OF INVENTION: POLYMORPHISMS IN THE HUMAN CARD4 GENE
FILE REFERENCE: 0734-386001
CURRENT FILING DATE: 2002-03-27
NOMBER OF SEQ 1D MOS: 121
SOFTWARE: FastSEQ for Windows Version 4.0
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57.0%; Pred. No. 27;
:ive 0: Mismatches
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. OTHER INFORMATION: Clone ID: 700963405H1
US-09-975-254-24327
                                                                                                   RESULT 8
8-09-97-52-54-24327
8-909-97-52-54-337, Application US/09975254
: GENEFAL INFORMATION:
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: OPGANISM: Homo sapiens
US-50-258-184-1
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US-60-358-184-1/c
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APPLICANT: Mannion, Jane
APPLICANT: Mannion, Jane
APPLICANT: Garger, Alexander
APPLICANT: Gordon, Brian
TILE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TILE OF INVENTION: COMPOSITIONS AND DIAGNOSIS OF KIDNEY CANCER
FILE REFERENCE: 210121.572
CURRENT APPLICATION NUMBER: US/10/102,524
CURRENT FILING DATE: 2002-03-19
NUMBER OF EQU ID NOS: 1863
SOFTWARE: FRASED for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 4.4%; Score 33; DB 5: Length 34762; Best Local Similarit; 53.5%; Pred. No. 8.5; Matches 59; Conservative 0; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 6: Length 272:
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                 APPLICANT: Rosen, et. al
TITLE OF INVENTION: Human Secreted Proteins
FILE REPERROCE: PS950
CURRENT APPLICATION NUMBER: US/10/105,299
CURRENT FILING DATE: 2002-03-26
NUMBER OF SEO ID NOS: 15197
Prior Application removed - See File Wrapper or Palm SOFTWARE: Patentin Ver. 2.0
LENGTH: 34762
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4.4%; Score 32.8; DB
Best Local Similarity 53.0%; Pred. No. 0.82;
Matches 70; Conservative 0: Mismatches
                                                                                                                                                                                                                                                                                                                  : NAME/KEY: misc_feature
... LOCATION: (19530)..(19530)
... OTHER INFORMATION: n equals a,t,g, or US-10-105-299-11849
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                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Homo sapiens
US-10-102-524-480
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2484 GGGAGGCCG 2476
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GENERAL INFORMATION:
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LENGIH: 272
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ITILE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PALOSPIO:
CURRENT APPLICATION NUMBER: US/10/102,806
CURRENT APPLICATION NUMBER: US/22
PRIOR PAPLICATION NUMBER: 09/925,298
PRIOR FILING DATE: 2001-08-10
PRIOR FILING DATE: 2001-08-10
PRIOR FILING DATE: 2001-08-0
PRIOR FILING DATE: 1990-03-08
PRIOR FILING DATE: 1990-03-08
PRIOR FILING DATE: 1990-03-12
NUMBER OF SEO ID NOS: 846
SOTHWARE: PATCHILIN VOF: 2.0
EDITOR FILING DATE: 1990-03-12
NUMBER OF SEO ID NOS: 846
SOTHWARE: PATCHILIN VOF: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cuery Match 4.2%: Score 31: DB 6: Length 6833; Pest Local Similarity 46.2%: Pred. No. 15: Matches 103: Conservative 0: Mismatches 120: Indels
                                                               Sequence 7027, Application US/10105299
SEMPAL INFORMATION:
FILE APPLICANT: Rosen, et. al
TITLE OF INVENTION: Human Secreted Proteins
FILE REFERENCE: PS950
GURRENT FILING DATE: 2002-03-26
NUMBER OF SEQ ID NOS: 15197
PTIOT Application removed - See File Wrapper or Palm
SEQ ID NO 7023
LEMSTH: 6833
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: GENERAL INFORMATION:
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OTHER INFORMATION: n equals
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US-10-105-299-7023
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ORGANISM: Homo sapiens
FEAIURE:
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LOCATION: (19)
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LCCATION: (20)
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LOCATION: (295)
                 RESULT 12
US-10-105-299-7023
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TILE OF INVENTION: Colon and Colon Cancer Associated Polynucleotijes and Polypertide UNREWITON: Colon and Colon Cancer Associated Polynucleotijes and Polypertide UNREWI APPLICATION NUMBER: US/10/106,598

PRIOR APPLICATION NUMBER: D00-03-27

PRIOR PILING DAIE: 2000-09-28

PRIOR FILING DAIE: 1999-09-29

PRIOR FILING DAIE: 1999-09-29

PRIOR FILING DAIE: 1999-09-29

PRIOR FILING DAIE: 1999-11-03

NUMBER OF SEQ ID NOS: 8564

SCOTIMARE: PATCHIN VAI. 3.0

SEQ ID NO 785

LENGTH: 555
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4.3%; Score 31.6; DB 5; Length 555;
Best Local Similarity 58.5%; Pred. No. 2.7;
Matches 55; Conservative 0; Mismatches 39; Indels
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TILE OF INVENTION: Human Polynucleotides and Polypeptides
FILE REFERENCE: 2546/1720
CURRENT APPLICATION NUMBER: US/09/789,189
FRIOR APPLICATION NUMBER: 60/183452
PRIOR APPLICATION NUMBER: 60/183452
PRIOR FILING DATE: 2000-02-18
NUMBER OF SEQ ID NOS: 2005
SOFTWARE: Patentin version 3.1
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4.2%; Score 31: DB 5: Length 255
Best Local Similarity 59.8%; Pred. No. 2.8;
Matches 52; Conservative 0: Mismatches 35: Indels
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Sequence 1604, Application US/09789189

GENERAL INFORMATION:
                                                            RESULT 10
US-10-106-558-786
: Sequence 786, Application US/10106598
: GENERAL INFORMATION:
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1071 AGTCAGGGGTGAGCA 1057
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; ORGANISM: Homo sapiens
US-10-106-658-786
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US-09-789-189-1604
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LENGIH: 256
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                                                                                                                      Length 748;
                                                                                                                                                      72: Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT PERLICATION NUMBER: US/10/105,299
CUPRENT FILING DATE: 2002-03-25
NUMBER OF SEQ ID NOS: 15197
Prior Application removed - See File Wrapper or Palm SEQ ID NO 12428
LENGTH: 49375
                                                                                                                   Score 30.8; DB 6;
Pred. No. 5.5;
0; Mismatches 72;
                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 15
US-10-105-299-12428/C
US-10-105-299-12428/C
Sequence 12428. Application US/10105299
SEQUENCE INFORMATION:
APPLICANT ESSEN, et. al
ITILE OF INVENTION: Human Secreted Proteins: FILE REFERENCE: PS950
                                                or
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       NAME/KEY: misc_feature
: LCCATION: (734)..(734)
: OIHER INFORMATION: n equals a,t,g,
US-10-106-698-1347
                                                                                                               Ouery Match
Best Local Similarity 50.7%;
Matches 74: Conservative
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; ORGANISM: HOMO :
US-10-105-299-12428
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ITLE OF INVENTION: Colon and Colon Cancer Associated Polynumismuses and Polypeptide FILE OF INVENTION: Colon and Colon Cancer Associated Polynumismuses and Polypeptide CURRENT APPLICATION NUMBER: US/10/106,598

CURRENT FILING DATE: 2002-03-27

PRIOR FILING DATE: 2000-09-28

PRIOR FILING DATE: 1999-09-29

PRIOR FILING DATE: 1999-11-03

NUMBER: OF SEQ ID NOS: 8564

SEQ ID NOS: 8564

SEQ ID NO 1347

LENGTH: 748
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51.2%; Pred. No. 5.2;
tive 0; Mismatches 62;
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OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc_feature
LOCATION: (512)
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LOCATION: (676)..(676) '
OTHER INFORMATION: n equals a,t,g, or
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                                                                                   LOCATION: (552)
OTHER INFORMATION: n equals a.t.g.
NAME/KEY: misc_feature
LOCATION: (558)
                                                                                                                                                                                                            OTHER INFORMATION: n equals a,t,q,
                                                    OTHER INFORMATION: n equals a, t, g, NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: n equals a,t,q,
NAME/KEY: misc_feature
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                                                                                                                                                          INFORMATION: n equals a,t,g,
                                                                                                                                                                                                                                                                OTHER INFORMATION: n equals a,t,g,
                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: n equals NAME/KEY: misc_feature LOCATION: (567)
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Best Local Similarity 51.21
Matches 65; Conservative
                                                                                                                                                                          NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: (588)
                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
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ORGANISM: Homo sapiens
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                                            April 19, 2002, 11:02:26; Search time 5830.82 Seconds
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/cgn2_6/ptodata/2/pna/US6001_COMB.seq.
/cgn2_6/ptodata/2/pna/US6002_COMB.seq.
/cgn2_6/ptodata/2/pna/US6003_COMB.seq.
/cgn2_6/ptodata/2/pna/US6004_COMB.seq.
/cgn2_6/ptodata/2/pna/US6005_COMB.seq.
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                  22023303 seqs, 10831430700 residues
                                                                                                                                                fotal number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                              nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                            Title:
Perfect score:
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                             OM nucleic
                                                                                          Sequence:
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/ cgn2_6/ptodata/2/pna/US6012_COMB.seq:*
/ cgn2_6/ptodata/2/pna/US6014_COMB.seq:*
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/ cgn2_6/ptodata/2/pna/US603_MERGED_COMB.seq:*
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/ cgn2_6/ptodata/2/pna/US602_MERGED_COMB.seq:*
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/ cgn2_6/ptodata/2/pna/US602_MERGED_COMB.seq:*
/ cgn2_6/ptodata/2/
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Description           | Segment 2 and 1 | 756            | 756         | 756           |                | ,<br>ע | , ,           | , ,         |             | 0       | 0       | 0            | 0.2   | . 7       | 148          | 140          | 150   | , ,          | 152          | 18. A         | 31,        | 46,           | 10                | 109,       | ě            | 17                | 49.       | 5,    | 23.              | 10               | Ś                |
|-----------------------|-----------------|----------------|-------------|---------------|----------------|--------|---------------|-------------|-------------|---------|---------|--------------|-------|-----------|--------------|--------------|-------|--------------|--------------|---------------|------------|---------------|-------------------|------------|--------------|-------------------|-----------|-------|------------------|------------------|------------------|
| ID                    | US-09-763-292-2 | -60-226-176-75 | -233-468-75 | -60-313-371-7 | -60-212-657-15 | -181-5 | -60-248-498-2 | 0-248-498-6 | -60-248-542 | 5-227-9 | 488-127 | 09-488-127B- | 486   | 182-895-1 | 60-182-895-1 | 60-182-895-1 | 82-89 | 50-182-895-1 | 60-182-895-1 | 60-198-818-18 | -60-213-79 | -60-213-795-4 | US-60-195-048-108 | 0-195-048- | -60-205-169- | US-60-198-818-178 | -671-317- | -60-2 | US-60-248-498-23 | US-60-245-227-10 | US-60-248-498-59 |
| DB                    | 30              | 55             | 99          | 64            |                |        |               |             |             |         |         |              |       |           |              |              |       |              |              |               | 54         | 24            | 25                | 25         | 53           | 25                | 56        | 55    | 57               |                  | 57               |
| Query<br>Match Length | 743             | 743            | 743         | 743           | 7609           | 32768  | 51955         | 222537      | 222537      | 225532  | 8437    | 8437         | 8437  | 572       | 572          | 572          | 572   | 572          | 572          | 572           | 58         | 1580          | 722               | 722        | 710          | 664               | 1001      | 32141 | 36191            | 36584            | 118047           |
| Query                 | 100.0           | 96.6           | 9.66        | 9.66          | ٣.             | ٦.     | ٣.            | ٣.          | ٣.          | m.      | œ       | œ            | œ     | œ.        | ∞.           | œ.           | æ     | æ.           | œ.           | œ.            | 73.2       |               | ٠.                | 71.7       |              | 65.7              | 58.4      |       | æ                | 58.4             | 58.4             |
| Score                 | 743             | 739.8          | 739.8       | 739.8         | 728.8          | 728.8  | 108           | 108         | 108         | 708     | 622.6   | 622.6        | 622.6 | 555.8     | 555.8        | 555.8        | 555.8 | 555.8        | 555.8        | 555.8         | 544.2      | 544.2         | 532.4             | 532.4      | 521.2        | 488 2             | 433.6     | 433.6 | 433.6            | 433.6            | 433.6            |
| Result<br>No.         | 1               | 2              | 3           | 4             | S              | 9      |               | ပ           |             | 10      |         |              | ۳,    | ₹1        | 'n.          |              | _     | m            | 6            | _             |            | 22            | 23                | C 24       | 57           | _                 | 27        | ~     | •                | _                | _                |
|                       |                 |                |             |               |                |        |               |             |             |         |         |              |       |           |              |              |       |              |              |               |            |               |                   |            |              |                   |           |       |                  |                  |                  |

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ptodata/2/pna/US6006\_COMB.seq:

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APPLICANT:

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Pred. No. 3.3e-209;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : Sequence 756, Application US/60226176
: GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                   ttgttagctcatgtgaagcgggg 743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; NAME/KEY: misc_feature
; OTHER INFORMATION: GB:HUM2C9X02
US-60-226-176-756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 99.6%;
Best Local Similarity 99.7%;
Matches 741; Conservative 0
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ 1D NO 756
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Pred. No. 3.7e-210;
Wismatches 0;
US-60-248-542-60

US-09-671-317-50

US-09-488-127-64

US-09-488-127-64

US-09-488-127-64

US-09-488-127-62

US-09-488-127-62

US-09-488-127-62

US-09-488-127-62

US-00-128-657-14

US-60-213-468-740

US-60-213-468-740

US-60-200-392-43

US-60-200-392-43
                                                                                                                                                                                                                                                                                                                                                                                       ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: AB Sangtec Medical
TITLE OF INVENTION: New method
FILE REFERENCE: primers
CURRENT APPLICATION INVERS: US/09/763,292
CURRENT FILING DATE: 2000-02-21
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/09763292 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
Best Local Similarity 100.0%;
Matches 743; Conservative 0;
     436
734
734
734
605
857
16238
654
1595
1595
  118047
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US-09-763-292-2
  RESULT 1
US-09-763-292-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 743
  4433.6
413.6
415.8
115.4
366.2
366.2
3466.2
331.2
331.2
331.2
325
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Sequence 756, Application US/60313371
GENERAL INFORMATION:
APPLICANT: Ring, Hujin Z.
APPLICANT: Malsen, Gareth
APPLICANT: Townley, David
APPLICANT: Morris, MacConald
ITILE OF INVENTION: Single Nucleotide Polymorphisms Associated With ADME C
FILE REFERENCE: GX-0013-5 p
CURRENT APPLICANT: US/60/313,371
CURRENT FILING DATE: 2001-08-16
NUMBER OF SEQ ID NOS: 2447
SCOTUMER: PERL Program
SEQ ID NO 756
                                                                                                                                                                                                                     Query Match 99.6%; Score 739.8; DB 64; Best Local Similarity 99.7%; Pred. No. 3.3e-209; Matches 741; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                         : NAME/KEY: misc_feature
; OTHER INFORMATION: GB:HUM2C9X02
US-60-313-371-756
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APPLICANT: Malsen, Gareth
APPLICANT: Townley, David
APPLICANT: Mortis, MacDonald
APPLICANT: Mortis, MacDonald
APPLICANT: Waldes, Ana
TITLE OF INVENTION: Single Nucleotide Polymorphisms Associated With ADME Genes
FILE REPERBECE: GX-0013-2 P
CURRENT APPLICATION NUMBER: U2/60/233,468
CURRENT FILING DATE: 2000-09-18
SOFTWARE: PERL Program
SED ID NO 756
LENGTH: 743
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APPLICANT:
Ring, Huijun Z.
                                                                                                                                                                           ; NAME/KET: misc_feature
; OTHER INFORMATION: GB:HUM2C9X02
US-60-233-468-756
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nes 741; Conservative
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ORGANISM: Homo sapiens
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Sequence 15, Application US/60212657
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN
TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN
TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN
TITLE OF INVENTION: DRUG-METABOLIZING PHASE I PROTEINS, AND USES THEREOF
CURRENT FILLING DATE: 2000-06-19
NUMBER OF SEQ ID NOS: 303
SEQ ID NOS: 303
SEQ ID NO 15
ENERGE FASLERO for Windows Version 4.0
ENERGE PARTITION OF THE PROTEINS AND USES THEREOF
ENERGY FALLING DATE: 2000-06-19
SEQ ID NO 15
ENERGY FALLING DATE: 2000-06-19
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                          98.1%; Score 728.8; DB 54; Length
llarity 99.6%; Pred. No. 2e-205;
Conservative 0; Mismatches 2; Indels
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CORGANISM: HUMAN
US-60-212-657-15
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Best Local Simil
Matches 741; C
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                           APPLICANT: Beasley, Ellen
IIIE OF INVENTION: ISOLATED HUMAN PHASE I DRUG-METABOLIZING
IIILE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUM
ITILE OF INVENTION: DRUG-METABOLIZING PROTEINS, AND USES THEREOF
CURRENT APPLICATION NUMBER: US/60/213,181
CURRENT FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 261
SEQ ID NO 56
LENGTH: 32768
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Sequence 56, Application US/60213181
GENERAL INFORMATION:
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: LOCATION: (1)...(32768)
: OTHER INFORMATION: n = ./
US-60-213-181-56
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ORGANISM: Human
FEATURE:
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TITLE OF INVENTION: ISOLATED HUMAN PHASE I DRUG-METABOLIZING
TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN
TITLE OF INVENTION: DRUG-METABOLIZING PHASE I PROTEINS, AND USES THEREOF
TITLE OF INVENTION: OWNERS. US/60/248,498
CURRENT APPLICATION NUMBER: US/60/248,498
CURRENT FILING DATE: 2000-11-15
SOFTWARE: FastSEO for Windows Version 4.0
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    Length 32768;
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Score 728.8; DB 5
Pred. No. 4e-205;
0; Mismatches 2
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APPLICATT: Beasley, Ellen
ITILE OF INVENTION: ISOLATED HUMAN
Match 98.1%;
Local Similarity 99.6%;
Hes 741; Conservative (
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Query Match
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ISOLATED HUMAN PHASE I DRUG-METABOLIZING
PROTEINS, NUCLEIC ACID MOLECULES ENCODING
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Pred. No. 8e-199;
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GENERAL INFORMATION:
APPLICANT: Beasley, Ellen
IIILE OF INVENTION: ISOLATED HUMAN
IIILE OF INVENTION: PROTEINS, NUCLE
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                                                        95.3%;
llarity 97.8%;
Conservative
                                A, I, C
TYPE: DNA

CRGANISM: HUMAN

FEATURE:

NAME/KEY: misc_feature

CATION: (1)...(51955)

COTHER INFORMATION: n = A,
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Best Local Similarity
Matches 728; Conserv
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   AND
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TITLE OF INVENTION: DRUG-METABOLIZING PHASE I PROTEINS, I FILE REPERBURE: CLOO0910 CURRENT APPLICATION WUMBER: US/60/248,498 CURRENT FILING DATE: 2000-11-15 WUMBER OF SEQ ID NOS: 264 SOFTWARE: Fast5EQ for Windows Version 4.0 SEQ ID NO 61 LENGHR 2223.7 TYPE: DNA CRANISM: HUMAN
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Pred. No. 1.6e-198;
0; Mismatches 15;
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                                                                                                or
                                                                               : NAME/KET: misc_feature
: LOCATION: (1)...(222537)
: OTHER INFORMATION: n = A,T,C
US-60-248-498-61
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Best Local Similarity 97.8%;
Matches 728; Conservative
                                                                         FEATURE:
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Ϊ PHASE 89893 90253 90193 90133 90073 90013 480 540 360 420 Gaps APPLICANT: Beasley, Ellen
TILLE OF INVENTION: ISOLATED HUMAN PHASE I DRUG-METABOLIZING
TITLE OF INVENTION: ISOLATED HUMAN PHASE ID BRUG-METABOLIZING
TITLE OF INVENTION: DRUG-METABOLIZING PROTEINS, AND USES THEREOF
FILE REFERENCE: CLO00946
CURRENT APPLICATION NUMBER: US/60/248,542
CURRENT APPLICATION NUMBER: US/60/248,542
NUMBER OF SEQ ID NOS: 342
SOFTWARE: FastSEQ for Windows Version 4.0 Length 222537; 1; Indels 15; Score 708; DB 57; Pred. No. 1.6e-198; 0; Mismatches 15; ; Sequence 62, Application US/60248542; GENERAL INFORMATION: or Ouery Match 95.3%; Best Local Similarity 97.8%; Matches 728; Conservative ( : NAME/KEY: misc\_feature : LOCATION 4...edf) ... (222537) : OTHER INFORMATION: n = A,T,C US-60-248-542-62 ORGANISM: Human 222537 TYPE: DNA LENGIH: 241 301 361 481 541 601 181 90192 90132 90072 90012 421 89952 89892 89772 qq ò q q DP Db ò ò qq ò qq ò ò g ò ò ò QQ ó

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LCCATION: (1)...(8437)
COTHER INFORMATION: n = A,T,C
US-09-488-127-59
                                                                                                                                                                                                                                                                                                                                                           Query Match 83.8°
Best Local Similarity 93.3°
Matches 694; Conservative
                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                RESULT 11
US-09-488-127-59
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TITLE OF INVENTION: ISOLATED HUMAN PHASE I DRUG-METABOLIZING
TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN
TITLE OF INVENTION: DRUG-METABOLIZING PHASE I PROTEINS, AND USES THEREOF
FILE REFERENCE: CLOOOB76
CURRENT APPLICATION NUMBER: US/60/245,227
CURRENT FILING DATE: 2000-11-03
NUMBER OF SEQ ID NOS: 129
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tgctaaatcaggcttagcaaatggacaaatagtaacttcgtttgctgttatctctgtct 120
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95.3%; Score 708; DB 57; Length 2

Best Local Similarity 97.8%; Pred. No. 1.6e-198;

Matches 728; Conservative 0; Mismatches 15; Indels
                                 or G
                                                                                         Sequence 9, Application US/60245227; GENERAL INFORMATION: APPLICANT: Beasley File
                                                                                                                                                                                                                                       NAME/KET: misc_feature

: LOCATION: (1)...(22532)

: OTHER INFORMATION: n = A,T,C

US-60-245-227-9
                                                                                                                                                                                                                TYPE: DNA ORGANISM: HUMAN
                                                                                                                                                                                                       LENGTH: 225532
                                                                                        US-60-245-227-9/c
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                                                                                                                                                                                               GENE STRUCTURE
                                                                                                                                                                                                                                                                                                                                                  83.8%; Score 622.6; DB 18;
93.3%; Pred. No. 9.7e-174;
Live 0; Mismatches 45; I
                                                                                                                                                           Sequence 59, Application US/0948B127
GENERAL INFORMATION:
APPLICANT: Thomann, Hans-Ulrich
APPLICANT: FitzGerald, Michael
ITILE OF INVENTION: USING CDNA SEQUENCE
FILE REFERENCE: 2709.1005-000
CURRENT APPLICATION NUMBER: US/09/48B.127
CURRENT FILING DATE: 2000-01-20
NUMBER OF SEQ ID NOS: 96
SOFTWARE: FastSED for Windows Version 4.0
SEQ ID NO 59
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| 2 | : LOCATION: 4305<br>: OTHER INFORMAT<br>: NAME/KEY: misc | DOCATION: 4332 DOCATION: 4356 DOTHER INFORMAT NAME/KEY: misc         | COATION: 4406 COATION: 4897 COTHER INFORMAT NAME/KEY: misc              | COCATION: 4906 COCATION: 4928 COTHER INFORMATION MAME/KEY INFORMATION MA | LOCATION: 5428<br>LOCATION: 5484<br>OTHER INFORMAT | LOCATION: 5514 LOCATION: 5514 OTHER INFORMATION NAME/KEY: misc                                     | LOCATION: 6718   LOCATION: 6718   LOCATION: 6781   LOCATION: 6791   LOCA | OTHER INFORMATION NAME/KEY: misc   | CATION: 6791 COTHER INFORMAT NAME/KEY: misc  | : LOCATION: 7370<br>: LOCATION: 7488<br>: OTHER INFORMAT | NAME/KEY: misc<br>  LOCATION: 7497<br>  LOCATION: 7528<br>  OTHER INFORMAT<br>  US-09-488-1278-59   | Query Match<br>Best Local Simil  | 1 1  |  | Db 1450 atctagte<br>Oy 121 acttccts  |   | Db 1569 catggtgg<br>03 241 gtttctgg  | Db 1629 gtttctg   |
|---|--|--|---|--|--|--|--|--|--|--|---|--|--|--|--|---|--|---|
|   | -  | Oy 541 ggggaagaggacttgaggaccqtgttcaagaggaagcccgctgcttgtggaggagtt 500 | Oy 601 gagaaaaccaagggtgggtgacctactccatatcactgaccttactggactactct 560<br> | Oy 661 tetetactgacattettggaaacattteagggtggecatatettteattatgagt-etg 719<br>   | Oy 720 gttgttagctcatgtgaagcgggg 743<br>            | RESULT 12<br>US-09-488-127B-59<br>; Sequence 59, Application US/09488127B<br>; GENERAL INFORMATION | APPLICANT: Thoman, Hans-Ulrich APPLICANT: FitzGerald, Michael S. ITLE OF INVENTION: RAPID DETERMINATION OF GENE STRUCTURE ITLE OF INVENTION: USING CDNA SEQUENCE   | FILE KEREKELE: 2/09.1U05-U00  CURRENT APPLICATION NUMBER: US/09/488,127B  CURRENT FILING DATE: 2000-01-20  NUMBER PS OF SEO 1D NOS: 97 | SOFTWARE: FartSE for Windows Version 4.0 SED ID NO 59 FORMARIES FOR SELECTION FOR SELE | TYPE: DNA CREANISM: Homo sapiens FRANTRE:                | NAME/KET: misc_feature<br>: LOCATION: 21, 33, 35, 45, 69, 70, 87, 129, 131, 153, 162, 169, 170,<br>: LOCATION: 217, 248, 448, 692, 869, 870, 871, 872, 873, 874, 875<br>: OTHER INFORMATION: n = A,T,C or G | : LOCATION: 876, 877, 878, 879, 880, 881, 882, 883, 884, 885, 886, 887, i. LOCATION: 949, 951, 1517, 2448, 2457, 2465, 2472, 2473, 2474  : OTHER INFORMATION: n = A.T.C or G  : NAME/RET: misc_feature | <ul> <li>JCCATION: 2475, 2476, 2477, 2478, 2479, 2480, 2481, 2482, 2483, 2484.</li> <li>JCCATION: 2485, 2486, 2487, 2488, 2489, 2490, 2491, 2492, 2493</li> <li>OTHER INFORMATION: n = A,T,C or G</li> <li>NAME/RET: misc_feature</li> </ul> | ; LOCATION: 2494, 2495, 2504, 2505, 2506, 2510, 2518, 2522, 2527, 2540.<br>; LOCATION: 2550, 2565, 2588, 2602, 2635, 2641, 2689, 3128<br>; OTHER INFORMATION: n = A,T,C or G<br>: NAME/KEY: misc feature | : LOCATION: 3380, 3381, 3382, 3383, 3384, 3385, 3386, 3387, 3388, 3389, COCATION: 3390, 3391, 3392, 3393, 3394, 3395, 3396, 3397, 3398 | . LOCATION: 3399, 3400, 3926, 3927, 3937, 3851, 4005, 4029, 4063, 4069, 10CATION: 4097, 4132, 4133, 4134, 4135, 4136, 4137, 4138, 4139, 4139, 10CATION: A WINDEMATION: n = A,T,C or G | : LOCATION: 4140, 4141, 4142, 4143, 4144, 4145, 4146, 4147, 4148, 4149, : LOCATION: 4150, 4157, 4174, 4177, 4191, 4193, 4195, 4201, 4203 ; OTHER INFORMATION: n = A,T,C or G | ; NAME/KET: misc_feature ,<br>; LOCATION: 4210, 4211, 4216, 4218, 4220, 4221, 4227, 4230, 4236, 4238, |

|                      | 4303,   | 4355,  | 4896,   | 4924,   | 5483,                      | 5513,  | 6702,                      | 6790,                      | 6790,   | 7487,                      | 7523,  | Gaps                           | ca 60<br> <br>ga 1449                  | ct 120<br>  <br>ct 1509             | acc 180<br>  <br>acg 1568               | ga 240<br>  <br>ga 1628       | tg 300<br>  <br>tg 1688            |
|----------------------|---|--|---|---|----------------------------|--|----------------------------|----------------------------|---|----------------------------|--|--------------------------------|--|-------------------------------------|---|-------------------------------|------------------------------------|
| 4272                 | 4301,   | 4350,  | 4895,<br>4905   | 4922,<br>5405   | 5482,<br>5492              | 5501,<br>5638  | 6701,<br>6780              | 6789,<br>6799              | 6789,<br>6799   | 7486,<br>7496              | 7521,  | 8437;                          | aaatat<br>        <br>aaatat           | ctctgt<br>      <br>ctgtat          | ctgaa<br>      <br>ctgga                | gaaga<br>     <br>gaagag      | gtagg<br>      <br>gtagg           |
| 4270,                | 4300,   | 4349,<br>4385,   | 4754,   | 4916,<br>5402,  | 5476,<br>5491,             | 5500,<br>5634,   | 6650,<br>6779,             | 6788,<br>6798,             | 6788,<br>6798,  | 7485,<br>7495,             | 7512,<br>8425  | Length<br>Indels               | tacaatga<br>         <br> tacaatga     | tgttat<br>     <br>tgttaa           | otgtattttggo<br>                        | atctt<br>       atctt         | aggatttg<br>                       |
| 4268,                | 4298,   | 4348,  | 4751,   | 4912,<br>5397,  | 5458,<br>5490,             | 5499,<br>5631,   | 6649,<br>6778,             | 6787,<br>6797,             | 6787,<br>6797,  | 7484,<br>7494,             | 7507,<br>8422,   | B 18;<br>174;<br>45; I         | <u> </u>                               | gtttgct<br>       <br> atttgct      |   | aggaagccctgattg<br>           | Cag                                |
| 4261,                | 4297,   | 4346,  | 4525,<br>4902,  | 4911,<br>5380,  | 5456,<br>5489,             | 5498,<br>5585,   | 6648,<br>6777,             | 6786,<br>6796,             | 6786,<br>6796,  | 7483,<br>7493,             | 7502,<br>8354,   | .6; DB<br>9.7e-1<br>ches       | aagcatacaa<br>                         | taacttcgt<br>         <br>tgacttcat | rtgttcacte<br>                          | gaagee<br>        <br> gaagee | gaaagagctaa<br>                    |
| 4256,                | 4296,   | 4345,  | 4491,   | 4910,<br>5372,  | 5439,                      | 5497,<br>5576,   | 6629,<br>6773,             | 6785,<br>6795,             | 6785,<br>6795,  | 7482,<br>7492,             | 7501,  | = 622<br>. No.<br>ismat        | ğ — ğ                                  | <u> </u>                            | cctg<br>                                | gtgad<br>     <br>gtgad       | ct = ct                            |
| 4254,<br>C or G      | 4292,<br>4317,<br>C or G                                | 4344,<br>4372,<br>C or G   | 4486,<br>4900,<br>C or G  | 4909,<br>5366,<br>C or G  | 5437,<br>5487,<br>C or G   | 5496,<br>5521,<br>C or G   | 6619,<br>6749,<br>C or G   | 6784,<br>6794,<br>C or G   | 6784,<br>6794,<br>C or G  | 7466,<br>7491,<br>C or G   | 7500,<br>8254,<br>c or G   | Score<br>Fred<br>0; M          | gtggctgaat<br>          <br>gtgactgaat | tggacaaaata<br>                     | ctatggc                                 | gaagca<br>     <br> gaagtg    | ttcccactgg<br>                     |
| , 4250,<br>- A,T,    | 4291,<br>4312,<br>A312,                                 | 4341,<br>4365,<br>- A,T,   | 4446,<br>4899,<br>AA,T,   | 4908,<br>5345,<br>A,T,  | 5434,<br>5486,<br>= A,T,   | 5495,<br>5516,<br>7 A,T,   | 6576,<br>6740,<br>A,T,     | 6783,<br>6793,<br>A,T,     | 6783,<br>6793,<br>A.T.  | m ~ :                      | 7499,<br>7544,<br>7541,  | 83.8%<br>93.3%<br>tive         | geetgt<br>       <br>geetgt            | tagcaaate<br>        <br>tagtaaate  | Jgt<br>Lat                              | gcatggatatgaag<br>            | aggcattttc<br>          aggccatttc |
|                      |   | 4338,<br>4360,<br>ION: n   | 4421,<br>4898,<br>ION: n  | . 4907,<br>. 5331,<br>ION: n  | 5433,<br>5485,<br>10N: n   | 5494,<br>5515,<br>10N: n   | 6501,<br>6733,<br>10N: n   | 6782,<br>6792,<br>10N: n   | 6782,<br>6792,<br>ON: n   | 7408,<br>7489,<br>ON: D    | 7498,<br>7531,<br>ON: n  | ল                              | rg — rg                                | caggett<br>[11111<br>caggett        | gctctcaaag<br>           <br>g-tctcaaaa | tgctgca<br>       <br>tgctgca | gaagagg<br>                        |
| : 42<br>FORM         | : misc_lea<br>1: 4285, 42<br>1: 4305, 43<br>1FORMATION: | : 4332<br>: 4358<br>FORMAT                                       | . 4408<br>: 4897<br>FORMAT  | . 4906<br>: 4928<br>: A928<br>FORMAT  | 5426<br>: 5484<br>FORMAT   | : 5493<br>: 5514<br>FORMAT   | 5645<br>: 6718<br>FORMAT   | 6791<br>6791<br>FORMAT     | 6781,<br>6791,<br>FORMATI   | 7370,<br>7488,<br>FORMATI  | 7497,<br>7528,<br>7528,<br>70RMATI   | h<br>Simila<br>94; Co          | cagaaatatttga<br>                      | ctaaatc<br>        <br>ctaagtc      | ttccta<br>                              | agtgg<br>     <br>ggtgg       | ttetg<br>      <br>ttetg           |
| LOCATION<br>OTHER IN | NAME/KEI<br>LOCATION<br>LOCATION<br>OTHER IN            | LOCATION: 4332, 431<br>LOCATION: 4358, 430<br>OTHER INFORMATION: | LOCATION: 440B, 4421, 4<br>LOCATION: 4897, 4898, 40<br>OTHER INFORMATION: n = 1<br>NAME/EFY: miss footing | LOCATION: 4906, 4907, 490 LOCATION: 4928, 5331, 534 OTHER INFORMATION: n = A, | CATION<br>CATION<br>HER IN | LOCATION: 5494, 5494, 5494<br>LOCATION: 5514, 5515, 551<br>OTHER INFORMATION: n = A,<br>NAMF/FFY: misc feature | CATION<br>CATION<br>HER IN | CATION<br>CATION<br>HER IN | LOCATION: 6781, 6782, 678. LOCATION: 6791, 6792, 679. OTHER INFORMATION: n = A.7 NAMP/KFV. misc feature | CATION<br>CATION<br>HER IN | MATCATION: 7497, 7498<br>LOCATION: 7528, 7531<br>OTHER INFORMATION: n<br>-09-488-127B-59 | ry Match<br>t Local<br>ches 69 | 1 tca<br>       <br>  391 tca          | 61 tgc<br> <br> <br> 450 atc        | 121 act<br>     <br>510 cct             | 181 cat<br>    <br>569 cat    | 241 gtt<br>    <br> 629 gtt        |
| _                    |   |  | :335 <b>2</b>   | 3352  | 3352                       | 3352   |                            |                            |   | 335                        |  | Query<br>Best<br>Match         | 0;<br>Db 1;                            | 0y.                                 | Oy 1                                    | 0y 19                         | Q; G                               |
|                      |   |  |   |   |                            |  |                            |                            |   |                            | _  |                                | ·                                      | V 12                                | · -                                     | ·                             | 0 1                                |

|   |  |  |                                      |   | N :   | Que<br>Bes<br>Mat  | Oy<br>Db  | oy<br>Dp  | Oy<br>Dp  | QY  |
|---|--|--|--------------------------------------|---|---|--|---|---|---|---|
| 301 tgcatgtgcctgtttcagcatctgtcttggggatgggat | 481 tggaaagaaatggaaggagttetetteetgttaggaatcgtttcagcaa 1855 481 tggaaagaaatggaaggagttecetetagaagaatcgttttcagcaa 1855 481 tggaaagaaatggaaggagttccectcatgacgctgcggaattttgggat 540 1867 tggaaagagatggaaggagtccggcgtttctccctcatgacgctgcgggaattttgggat 1926 541 ggggaaagagagtattgaggaccgtgttcaagaggaagccgctgctgtggaagagtt 600 1911 | gagaaaaccaaggggggggcctactccatatcactgcctactggactactct 660 | 720 gttgttagctcatgtgaagcgggg 743<br> | Sequence 97, Application US/09488127B Sequence 97, Application US/09488127B Sequence 97, Application US/09488127B GENERAL INFORMATION: APPLICANT: Thomann, Hans-Ulrich APPLICANT: Thomann, Hans-Ulrich APPLICANT: Thomann, Hans-Ulrich APPLICANT: Thomann, Hans-Ulrich TITLE OF INVENTION: RAPID DETERMINATION OF GENE STRUCTURE TITLE OF INVENTION: USING CDNA SEQUENCE FILE REPERENCE: 2709.1005-000 CURRENT APPLICATION NUMBER: US/09/488,127B CURRENT APPLICATION NUMBER: US/09/488,127B CURRENT FILE SEQUENCE: 2000-01-20 SEQUINGER OF SEQUENCE: 2000-01-20 SEQUENCE: APPLICATION ONS: 97 LIENGTH: 8437 TYPE: DNA ORGANISM: HOMO sapiens | NAME/REY: misc_feature<br>LOCATION: 13, 16, 84, 164, 184, 894, 907, 910, 915, 917, 926, 931,<br>LOCATION: 936, 937, 938, 939, 940, 941, 942, 943, 944, 945, 946<br>NAME / INCOMENTION: n = A,T,C or G | LOCATION: 947, 948, 949, 950, 951, 952, 953, 954, 955, 956, 972, LOCATION: 1005, 1030, 1068, 1639, 1640, 1641, 1642, 1644  LOCATION: 1005, 1030, 1068, 1639, 1640, 1641, 1642, 1644  NAME IN PROPARATION: n = A,T,C or G | LOCATION: 1645, 1646, 1647, 1648, 1649, 1650, 1651, 1652, 1653, 1654, LOCATION: 1655, 1656, 1657, 1658, 1659, 1660, 1661, 1665, 1689  MARIER INFORMATION: n = A,T,C or G  MANAPARET INFORMATION: n = A,T,C or G | CCATION: 1698, 1705, 1720, 1736, 1737, 1787, 1788, 1789, 1790, 1809, LOCATION: 1819, 1862, 1937, 2793, 2804, 2807, 2853, 2862 OTHER INFORMATION: n = A,T,C or G | LOCATION: 2917, 2922, 2923, 2924, 2925, 2937, 2938, 2939, 2940, 2941, LOCATION: 2942, 2943, 2944, 2945, 2946, 2947, 2948, 2949, 2950  OTHER INFORMATION: n = A,T,C or G | namic/AEI: MilsC_leadure<br>LOCATION: 2951, 2952, 2953, 2954, 2955, 2956, 2962, 2980, 2982, 2999, |
| oy oy                                       | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0  | 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6                    | 0 <b>3</b>                           | RESULT Seque Seque GENE GENE APPI TITI FILIT FILIT FILIT SEQ I SEQ I  |   |  |   |   |   |   |

|                              |  |                                      |  |   |  |   |   |  |   |  |  |   | 4<br>                          |   |   |  |   |
|------------------------------|--|--------------------------------------|--|---|--|---|---|--|---|--|--|---|--------------------------------|---|---|--|---|
|                              | 527,   | 913,                                 | 092,   | 141,  | 217,   | 293,  | 487,  | 053,   | 928,  | 158,   | 54,  | ,06   | Gaps                           | 60  | 120                                       | 180<br>1568                                    |   |
|                              | ж  | ě,                                   | 4  | 4   | 4  | ¥   | <b>*</b>  | . 20   | . 59  | , 59   | 75   | 81  | ••                             | tca<br>   <br>  tga                               | tet<br>tet                                | acc<br>acg                                     |   |
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| 3041,                        | 3516,<br>3534,   | 3543,<br>4053,                       | 4088,<br>4111,   | 4137,   | 4202,  | 4290,   | 4375,<br>5041,  | 5050,<br>5749,   | 5911,<br>5946,  | 5955,<br>5965,   | 7551,<br>7561,   | 7569,<br>8309,  | 5                              | Saaata<br>       <br>Saaata                       | jtttgc<br>     <br> tttgc                 | ctgtattttgg<br>                                |   |
| 3036,                        | 3514,<br>3533,   | 3542,<br>4051,                       | 4083,<br>4107,   | 4135,<br>4166,  | 4200,  | 4289,<br>4299,  | 4369,<br>5040,  | 5049,<br>5310,   | 5898,<br>5945,  | 5954,  | 7489, 7560,  | 7568,<br>8307,<br>8417                                    | ); DB<br>).7e-17               | gcatad<br>      <br> gcatad                       | acttco<br>                                | さニさ  |   |
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| 3012,<br>or G                | <i>C C C</i>   | 3540,<br>4017,<br>or G               | 4078,<br>4100,<br>or G   | 4132,<br>4151,<br>or G  | 1195,<br>1227,<br>or G                       | 4281,<br>4297,<br>or G  | 4306,<br>5038,<br>or G  | 5047,<br>5057,<br>or G   | 5873, 1<br>5943, 1<br>or G  | 5952,<br>5962,<br>or G   | 6921, 7<br>7558, 7<br>or G   | 7566, 7<br>8276, 8<br>or G<br>8403, 8                     | Score<br>Pred.<br>0; Mis       | agcctgtgtggctgaataaaagcatacaaatacaatgaaatatca<br> | gacaaa<br>                                | ggtctatggccctgtgttca<br>                       |   |
| 3005,<br>A, T, C             | 3093,<br>3530,<br>A, T, C                                    | 3539,<br>3992,<br>A,T,C              | 073,<br>097,<br>A, T, C  | 126,<br>147,<br>A, T, C   | 188,<br>222,<br>A, T, C                      | 264,<br>296,<br>A, T, C   | 305,<br>512,<br>A, T, C   | 046,<br>056,<br>A, T, C  | 850,<br>934,<br>A, T, C   | 51,<br>61,<br>,T,C   | 90,<br>57,   | 65,<br>,T,C<br>,T,C<br>,T,C                               | 3.8%;<br>3.3%;<br>Ve           | ctgtgt<br>        <br>ctgtgt                      | gcaaatgg<br>         <br>gtaaatgg         | aggtet<br>      <br>aaatet                     |   |
| 04,<br>n                     | 83,<br>29,<br>n  |                                      | . 4066, 4<br>, 4094, 4<br>ION: n =                                   | 121, 4<br>121, 4<br>146, 4  | 4184, 4<br>4184, 4<br>4220, 4<br>N: n =      | ature<br>261, 4<br>295, 4   | 304, 4<br>304, 4<br>511, 4  | atures<br>045, 5<br>055, 5   | 336, 58   | atures<br>950, 5<br>960, 5   | utures<br>181, 5<br>556, 7   | atures<br>564, 7<br>268, 8<br>: n = .<br>atures<br>369, 8 | 83<br>ity 93<br>servativ       |   | cttag<br>      <br> cttag                 | agctctcaaaggt<br>            <br>ag-tctcaaaaat |   |
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TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING INTILE OF INVENTION: DRUG-METABOLIZING PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
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TITLE OF INVENTION: AND USES THEREOF
CURRENT APPLICATION NUMBER: US/60/182,895
NUMBER OF SEQ ID NOS: 590
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SEQ ID NO 147
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TITLE OF INVENTION: ISOLATED HUMAN DRUG-METABOLIZING
TITLE OF INVENTION: ISOLATED HUMAN DRUG-METABOLIZING
TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING ITILE OF INVENTION: DRUG-METABOLIZING PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL000262
CURRENT PPLICATION NUMBER: US/60/182,895
CURRENT FILING DATE: 2000-02-16
NUMBER OF SEQ ID NOS: 590
SOCTHARE: FASLSEQ for Windows Version 4.0
SEQ ID NO 148
LENGTH: 572
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L16881 Homo sapien

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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                               HUM2C9X05 323 bp DNA PRI 08-FE Homo sapiens cytochrome P4502C9 (CYP2C9) gene, exon 7. L16881.1 G1:291611 CYP2C9: cytochrome P450; mephenytoin 4-hydroxylase.
                                                                                                                                                                                                                                                                                                                                                    ALIGNMENTS
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AL359672
AC018872
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AR071576
HUMCYP2C9
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M61856 Human cytoc AR071577 Sequence AR071580 Sequence M61853 Human cytoc

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SUMMARIES

Cloning and expression of complementary DNAs for multiple members of the human cytochrome P450IIC subfamily Biochemistry 30, 3247-3255 (1991) 91182740 1 (sites)
Goldstein,J.A., Raucy,J.L., Blaisdell,J.A., Faletto,M.B. and (bases 1 to 323) REFERENCE AUTHORS MEDLINE REFERENCE JOURNAL TITLE

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de Morais,S.M., Schweikl,H., Blaisdell,J. and Goldstein,J.A.
Gene structure and upstream regulatory regions of human CYP2C9 and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens chromosome 10 clone RPI1-208C17, *** SEQUENCING IN PROGRESS ***, 2 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (26-JUN-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jun 28, 2001 this sequence version replaced gi:14529836.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 gcatgcaagacaggagccacatgccctacacagatgctgtgtgcacgaggtccagagat 180
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AL3S9672.17 GI:14575223
HTG: HTGS_PHASEI; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP.
                                                                                 /organism-"Homo sapiens"
/db.xref-"taxon:9606"
/tissue_type-"liver"
/tissue_lib-"EMBL3 library from J.A. Goldstein"
70. 257
                                                                                                                                                                                                                                                                                                 0;
                                   Biochem. Biophys. Res. Commun. 194 (1), 194-201 (1993) 93326116
                                                                                                                                                                                                                                                                        Length 323;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 143087)
Johnson,C.
                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                   100.0%; Score 323; DB 9;
100.0%; Pred. No. 1.5e-84;
ive 0; Mismatches 0;
                                                                                                                                                                                                                       93
                                                                                                                                                                                                          /evidence=experimental
                                                            Location/Qualifiers
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                                                                                                                                                                                   /citation=[1]
/number=7
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Best Local Similarity 100.
Matches 323; Conservative
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                        CYP2C18
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AUTHORS
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Center code: SC

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99506 CCCTGAATIGCTACAACAAAIGTGCCATITITCTCCTTITCCATCAGTITITACTIGIG 99565
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                                                                                         Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08755; 100% of reads
Sequencing vector: plasmid; L08755; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 142866 bases at least 040
Consensus quality: 142804 bases at least 030
Consensus quality: 142920 bases at least 020
Insert size: 142987; sum-of-contigs
Insert size: 142987; sum-of-contigs
Quality coverage: 8.55x in 020 bases; sum-of-contigs Quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              * NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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/note="assembly_fragment:00967"
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/note="assembly_fragment:00494
                                                   Center project Information
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/Organisme*Homo sapiens*
/Organisme*Thomo sapiens*
/Organisme*Thomo sapiens*
/Chromosome=*10*
/clone=*RP11-208C17*
Web site: http://www.sanger.ac.uk
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                             Contact: humquery@sanger.ac.uk
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47106. .143087
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KEYWORDS
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 173154)
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Submitted (03-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
On Jun 28, 2001 this sequence version replaced gi:14456168.
                                      04-JUL-2001
*** SEQUENCING IN
                                                                                                                                                                                                                                                                                                                                                                                                         Assembly program: XGR44; version 4.58
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 172989 bases at least 040
Consensus quality: 173145 bases at least 030
Consensus quality: 173145 bases at least 020
Insert size: 173154; sum-of-contigs
Insert size: 116005; 33.1% error; agarose fp
Quality coverage: 6.48x in 020 bases; sum-of-contigs Quality
coverage: 9.80x in 020 bases; agarose-fp
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                                                                                    AL13513.11 GI:14575067
HTG: HTGS_PHASE2: HTGS_ACTIVEFIN: HTGS_DRAFT: HTGS_FULLTOP.
human.
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* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

Location/Qualifiers

1. 173154
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                                    HOMO Sapiens chromosome 10 clone RP11-400G3, PROGRESS ***, in ordered pieces.
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92.6%; Pred. No. 3.4e
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                            Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                              Center code: SC
Web site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="10"
/clone="RP11-400G3"
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1. 173154
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                               173154 bp
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Best Local Similarity
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                               AL133513
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Mashreghi. Wohammadi, M.

Direct Submission

L Submitted (11-JUN-2001) Sanger Centre, Hinxton, Cambridgeshire, CBLO 15A, UK. E-mail enquiries: humquery@sanger.ac.uk
on Jun 14, 2001 this sequence version replaced gi:14148873.
Center: Sanger Center
Center: Sanger Center
Center: Canger Center
Center code: SC
Web Site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
Contact: humquery@sanger.ac.uk
Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                    HOMO Sapiens chromosome 10 clone RP11-466J14, *** SEQUENCING IN PROGRESS ***, 2 unordered pieces.
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Assembly program: XARP4: version 4.5
Assembly program: XARP4: version 4.5
Sequencing vector: plasmid: L08752; 100% of reads
Consensus quality: 205236 bases at least Q40
Consensus quality: 205448 bases at least Q30
Consensus quality: 205560 bases at least Q30
Insert size: 205691; sum-of-contigs
Insert size: 188405; 9.1% error; agarose-fp
Quality coverage: 11.31x in Q20 bases; sum-of-contigs Quality
coverage: 12.57x in Q20 bases; agarose-fp
                                                                                                           actatctcattcccaaggtaagtttgtttctcctacactgcaactccatgttttcgaagt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALSB3B36.11 GI:14455940
HIG; HIGS_PHASE1; HIGS_ACTIVEFIN; HIGS_DRAFT; HIGS_FULLTOP
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is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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88341 205791: contig of 117451 bp in length.
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Mammalia: Eutheria: Primates;
1 (bases 1 to 205791)
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de Morais, S.M., Schweikl, H., Blaisdell, J. and Goldstein, J.A.
Gene structure and upstream regulatory regions of human CYP2C9 and
                                                                                                                                                                                                                                                                                                                                                                                                                              154954
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Mammalla: Eutheria: Primates; Catarrhini; Hominidae: Homo.
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Correction: Cloning and expression of complementary CDNAs for multiple members of the human cytochrome P450IIC subfamily Biochemistry 32, 1390-1390 (1993)
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Goldstein,J.A., Raucy,J.L., Blaisdell,J.A., Faletto,M.B. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 actatctcattcccaaggtaagtttgtttctcctacactgcaactccatgttttcgaagt
                                                                                                                                                                                                                     Length 205791;
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Homo sapiens cytochrome P4502C18 (CYP2C18) gene, exon 7.
L16874
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Romkes.N., Faletto,M.B., Blaisdell,J.A., Raucy,J.L. and
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                                                                                                              100 others
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                                                                                                                                                                                                                        DB 2;
                                                                                                                                                                                                               85.2%; Score 275.2; DB 2 92.6%; Pred. No. 3.4e-70; ive 0; Mismatches 23
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38262 c 40890 g 69845 t

    .348.
    /organism="Homo sapiens"

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Matches 300; Conservative
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Homo sapiens
Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria: Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 156492)
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Direct Submission
Submitted (05-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire, Submitted (05-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 15A, Wr. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jul B, 2001 this sequence version replaced gi:14586042.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             242
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Homo sapiens chromosome 10 clone RP11-361K9, *** SEQUENCING IN
PROGRESS ***, in ordered pieces.
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                                                                                                                                                                                                                                                                                                                                                     62
                                                                                                                                                                                                                                                                                                                                                                                    93
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                                                                                                                                                                                                                                                                                                                                                            HTG: HTGS_PHASE2; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP
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Web site: http://www.sanger.ac.uk
                                                                                                                                                                                      /evidence=experimental
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AL157835.9 GI:14626943
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 143087)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63 ttatcagctaaagtccaggaagagattgaacgtgtgattggcagaaaccggagccctgc 122
Sequencing vector: plasmid; L08752; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Consensus quality: 156104 bases at least 040 Consensus quality: 156104 bases at least 030 Consensus quality: 156216 bases at least 030 Insert size: 156492; sum-of-contigs Insert size: 156492; sum-of-contigs Insert size: 150975; 13.7% error: agarose-fp Quality coverage: 8.34x in 020 bases; sum-of-contigs Quality coverage: 9.69x in 020 bases; agarose-fp
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* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

Location/Qualifiers
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HTG: HTGS_PHASE1: HTGS_ACTIVEFIN: HTGS_DRAFT: HTGS_FULLTOP.
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91.7%; Pred. No. 1.3e-66;
tive 0; Mismatches 25
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Best Local Similarity 91.74
Matches 289; Conservative
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On Jun 28, 2001 this sequence version replaced g1:14529836.
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                                                                                                                                                                                                                                       Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 14266 bases at least 040
Consensus quality: 142843 bases at least 030
Consensus quality: 142920 bases at least 020
Insert size: 142897; sum-of-contigs
Insert size: 142897; sum-of-contigs
Ouality coverage: 8.55x in 020 bases; sum-of-contigs Quality
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          182 ccttgaccttctccccaccagcctgcccatgcagtgacctgtgacattaaattcagaaa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100 others
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Best Local Similarity 83.2%; Pred. No. 1.2e-54;
Matches 253; Conservative 0; Mismatches 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 coverage: 7.82% in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vector_side:left"
47106. .143087
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a 26155 c 27788 g 47797 t
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1 47005
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                                                                                                                                                                           Web site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
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                                                                                                              Center: Sanger Centre
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LOCUS

RESULT AC018872

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REFERENCE AUTHORS TITLE

JOURNAL REFERENCE AUTHORS

TITLE

COMMENT

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g of 12178 bp in length
f unknown length
g of 9855 bp in length
f unknown length
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contig of 14046 bp in length
gap of unknown length
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contig of 22766 bp in length
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                                                                                                                                                                                                                                                                                                             of 8460 bp in length
unknown length
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of 4779
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of 7469
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of 7177 h
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of 8460 h
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                                                              of 3268
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    /organism="Homo sapiens"
/db_xref="taxon:9606"
    /chromosome="2"

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                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (21-DEC-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Feb 18, 2001 this sequence version replaced gi:8954228.
                                                                                                                                                                                                  Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 201340)

Waterston, R. H.
Db 18016 CTACCTCATCCCCAAGGTAAGCTTGTTTCTCTTACACTATATTTCTGTACTTCTGAAATT 17957
                                                                                                                AC018872 201340 bp DNA HTG 18-FEB-2001
HOMO sapiens chromosome 2 clone RP11-140M22, WORKING DRAFT
SEQUENCE, 28 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOTE: This is a 'working draft' sequence. It currently consists of 28 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                      Center: Washington University Genome Sequencing Center
Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                          ---- Genome Center
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bp in length
length
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1502: gap of unknown length
2841: contig of 1339 bp in length
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gap of unknown length
contig of 2776 bp in length
gap of unknown length
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unknown length
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[1810
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                                               Db 17956 TCCA 17953
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VERSION
KEYWORDS
SOURCE
ORGANISM
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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DD 116925 TACCTCCCCAAGGTAAGCTTGTTTCTCCTAGACTGTGCGTCTATGCTCTTGATGTC 116984
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2 clone RP11-358N5 map 2, WORKING DRAFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     183 cttgaccttctccccaccagcctgccccatgcagtgacctgtgacattaaattcagaaac
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0; Mismatches 52;
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46006. 50784
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Matches 264; Conservative
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RENET I Thousage in Controlate; Cranista, Vertebrate; Euteleostomi; Renet and Relation Charles.

RENET I Thousage in Co. 2009; Immunes; Catterfinii, Nominidae; Nomo.

BITCH I LINCOLL. Nusbaum.C. and Lander.E. Allen.N. Anderson.N. BITCH I LINCOLL. Nusbaum.C., Lander.E., Allen.N. Anderson.N., Bailor I Lincoll. No. 2009; Immunes; Catterfinii, Doublant.L. Boyle.N., Castala.A. Castala.A. Collinis.S. Collymore.A.

BITCH I LINCOLL. Nusbaum.C., Lander.E., Allen.N. Anderson.N., Bailor.D. Castala.A. Castala.A. Collinis.S. Collymore.A.

BITCH I LINCOLL. Nusbaum.C., Lander.E., Mann.L., Rattas.N. Klein.J. Lebocaty.J. Castala.A. Collinis.S. Collymore.A.

Baidoli.J. Castala.A. Collingelo.N. Collinis.S. Collymore.A. Klein.J. Lebocaty.J. Castala.A. Collinis.S. Collymore.A. Klein.J. Lebocaty.J. Lieu.C. Locke.N. MacCaptala.N. Marquis.N. Collinis.S. Callymore.A. Klein.J. Lebocaty.J. Lieu.C. Locke.N. Stantol. Comment.P. Mortrow.J. Navior.J. Norman.C.H. O'Connor.T. O'Connor.T. Collinis.J. Ned Forty.P. Stantol. Collinis.D. Norman.C.H. O'Connor.T. O'Connor.T. Collinis.J. Ned Forty.P. Stantol. Collinis.J. Ned Forty. Stantol. Collinis.J. Ned Forty. Stantol. Collinis.J. Ned Forty. Stantol. Collinis.J. Norman.C.H. O'Connor.T. O'Connor.T. Collinis.J. Ned Forty.P. Stantol. Collinis.J. Ned Forty. Stantol. Collinis.J. Norman.C.H. O'Connor.T. O'Connor.T. O'Connor.T. Collinis.J. Ned Forty.P. Stantol. Collinis.J. Norman.C.H. O'Connor.T. O'Connor.T. O'Connor.T. Collinis.J. Norman.C.H. O'Connor.T. O'Connor
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126994 127093: gap of 100 bp 11 length 127094 139959: contig of 12866 bp in length 139960 140059: gap of 100 bp 140060 155880: contig of 15821 bp in length 155881 155980: contig of 15821 bp in length 170719: contig of 14739 bp in length 170720 170819: gap of 100 bp 170820 200516: contig of 29697 bp in length 200517 200616: gap of 100 bp 200517 200616: gap of 1000 bp 200517 200616: gap of 1000 bp 200517 200618: gap of 1000 bp 200518: gap of 1000 
99 24398: gap of 100 bp
99 29876: contig of 5478 bp in length
77 29976: app of 100 bp
77 36607: contig of 6631 bp in length
88 36707: gap of 100 bp
8 43142: contig of 6435 bp in length
13 4321: gap oft 100 bp
13 49210: contig of 5968 bp in length
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contig of 5968 bp in length
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/clone_lib="RPCI-11 Human Male BAC"
1. 5808
/note="assembly_fragment
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/note="assembly_fragment"
55981. 63850
/note="assembly_fragment"
63951. 71005
/note="assembly_fragment"
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/note="assembly_fragment"
36708. .43142
/note="assembly_fragment"
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note="assembly_fragment"
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/note="assembly_fragment"
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/note="assembly_fragment"
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/note="assembly_fragment"
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'note="assembly_fragment"
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note="assembly_fragment"
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80802. .126993
/note="assembly_fragment"
127094. .139959
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/db_xref="taxon:9606"
/chromosome="2"
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80701: cont
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Rabbit cytochrome P450IIC5 (CYP2C5) gene, exon 7.
M74204.1 GI:165568
Cytochrome P450 IIC5; drug metabolism; microsomal membrane protein; monooxygenase.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
H (bases 1 to 595)
Zhao, J., Chan, G., Govind, S., Bell, P. and Kemper, B.W.
Structure of 5' regions and expression of phenobarbital-inducible ababit cytochrome P450IIC genes
DNA Cell Biol. 9, 37-48 (1990)
                                                                                                                                                                                                                                                                   4; Gaps
                                                                                                                                                                                                                 Length 210821;
                                                                                                                                                           2111 others
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37637 c 36968 g 66777 t
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/organism="Oryctolagus cunics/
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/tissue_type="liver"
/dev_stage="adult"
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/note="assembly_fragment"
155981. .170719
/note="assembly_fragment"
170820. .200316
/note="assembly_fragment"
200617. .210821
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Best Local Similarity
Matches 192; Conserv
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Goldstein J.A. and De Morais, S.M.F.
Goldstein J.A. and dagnosis of human cytochrome P450 2C19:
the principal determinant of s-mephenytoin metabolism
Patent: US 5912120-A 4 15-JUN-1999,
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100.0%; Pred. No. 7.3e-46;
1ve 0; Mismatches 0; Indels (
                                                        Length 595;
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Pred. No. 1.7e-46;
0; Mismatches 55
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Seguence 4 from patent US 5912120.
ARU71576
               /evidence-experimental
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/gene="CYP2C5"
/number=7
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Best Local Similarity 81.0%;
Matches 23%; Conservative
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Best Local Similarity 100.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
Eutheria; Primates; Catarhini; Hominidae; Homo.
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Biochemistry 30 (13), 3247-3255 (1991)
                                                                                                                             Eukaryota: Metazoa; Chordata: Craniata; Vertebrata; Euteleostomi: Mammalia: Eutheria: Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 1854)
Romkes.M., Faletto,M.B., Blaisdell,J.A., Raucy,J.L. and Goldstein,J.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1091 ACCTICTCCCCACCAGCCTGCCCCATGCAGTGACCTGTGACATTAAATTCAGAAACTATC 1150
     31-DEC-1994
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100.0%; Pred. No. 7.3e-46;
iive 0; Mismatches 0;
                 Human cytochrome P4502C9 (CYP2C9) mRNA,
M61855 J05326
M61855.1 GI:181301
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                                                                       cytochrome P450; cytochrome P450 2C9 Human, cDNA to mRNA. Homo sapiens
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02-SEP-2000 (Rel. 65, Last updated, Version
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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/gene="CYP2C9"
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Ohgiya, S., Komori, M., Ohi, H., Shiramatsu, K., Shinriki, N. and
 Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                                                   Homo sapiens (human)
JP 1996056695-A/2
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                                                                                                                                                   topology: Linear;
hypothetical: No;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human liver.
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KEYWORDS
SOURCE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
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                                                                                                                                                                                                                                                                               Gaps
                                                                               FUNAE YOSHIHIKO, IMAOKA SUSUMU, MATSUKI YASUSHI, HAYASHI KOJI.
                                                                                      YABUSAKI YOSHIYASU
COTK16/18,C12N15/09,G01N33/53,G01N33/53//C12N1/19,C12N9/02.
(C12N1/19,
                                                                                                                                                                                                                                                                Length 1473;
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              Funae I., Imaoka S., Matsuki Y., Hayashi K., Yabusaki Y.;
*AMTIBODY RECOGNIZING CYTOCHROME P4502C9 ORIGINATED FROM MAN";
Patent number JP1996027196-A/5, 30-JAN-1996.
SUMITOMO CHEM CO LTD.
                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                         Sequence 1473 BP; 413 A; 345 C; 319 G; 396 T; 0 other;
                                                                                                                                                                                                                                                               58.9%; Score 190.4; DB 22; 99.5%; Pred. No. 2.1e-45; ive 0; Mismatches 1;
                                                                                                                                                                              /product-"cytochrome P4502C9"
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1. .1473
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02-SEP-2000 (Rel. 65, Last updated, Version
                                                                                                                                                                                                            1. .1473
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                                                                                                                                   Location/Qualifiers
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                                                                                                                                                                                              Location/Qualifiers
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                                                                         13-JUL-1994 JP 1994161551
                                                                                                                    strandedness: Double;
                                                   sapiens (human)
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Best Local Similarity 99.5
Matches 191; Conservative
                                                         JP 1996027196-A/5
30-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                         1139 TCATTCCCAAGG 1150
                                                                                                                             copology: Linear;
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                                                                                                            C12R1:865);
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Homo sapiens
Sukaryota: Metazoa; Chordata: Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo
1 (bases 1 to 1814)
Yabusaki Y., Komai K., Kaneko H., Nakatsuka I.;
SAFEIY";
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putative CYPC2C9 gene [human, liver, mRNA, 1814 nt].
S46963
S46963.1 GI:258514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 58.9%: Score 190.4; DB 22; Length Best Local Similarity 99.5%; Pred. No. 2.1e-45; Matches 191; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                          15-JUL-1994 JP 1994164184
20-JUL-1993 JP 93P 201120, 30-JUL-1993 JP 93P 2
17-JUN-1994 JP 94P 136053
HAYASHI KOJI, SAKAKI TOSHIVUKI, YABUSAKI YOSHIYASU, KOMAI KOICHIRO, NAKATSUKI IWAO
C1201/02.C1ZM1/34,C1201/26;
strandedness: Double;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP; 413 A; 345 C; 319 G; 396 T; 0 other;
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  Hayashi K., Sakaki T., Yabusaki Y., Komai K.
*METHOD FOR EVALUATING SAFETY*;
Patent number 191996056695-A/2, 05-MAR-1996.
SUMITOMO CHEM CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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/organism="Homo sapiens"
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| Journal of the Care of the C
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;
Ramataki,T.
Six-base deletion occurring in messages of human cytochrome P-450
in the CYP2C subfamily results in reduction of tolbutamide
                                                                                                                                                                                                                      GenBank staff at the National Library of Medicine created this entry (NCBI gibbsq 117179) from the original journal article. This sequence comes from Fig. 1.
Author also gives sequence for another cytochrome P-450 that contains a 6-base deletion of nucleotides 783-788.

Location/Qualifiers
1.1814
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Best Local Similarity 99.5%; Pred. No. 2.2e-45;
Matches 191; Conservative 0; Mismatches 1: Indels 0;
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Blochem. Int. 27 (6), 1073-1081 (1992)
93075249
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Search completed: April 19, 2002, 09:34:57 Job time: 7997 sec

| US-09-172-711-5<br>US-08-750-703-1<br>US-08-750-703-1<br>US-08-145-58D-14<br>US-08-145-58D-14<br>US-08-145-58D-22<br>US-08-145-58D-15<br>US-08-145-58D-16                | 62.2 19.3 1666 2<br>62.2 19.3 1666 2<br>61.2 19.3 1568 2<br>61 18.8 237 2<br>56.6 17.5 1501 2 | 52 16.1 189 6 5508199-9<br>39.2 12.1 6387 1 US-07-721-775A-1<br>39.2 12.1 6387 1 US-08-339-658-1   | ALIGNMENTS  | 201-118-4<br>ence 4, Api<br>nt No. 578(<br>ERAL INFORM | : APPLICANT: GOLDSTEIM, JOYGE A : APPLICANT: GONKES-SPARKS, Marjorie : ITILE OF INVENTION: DIAS FOR MULTIPLE MEMBERS OF THE HUMAN CITOCHROME P450 2C : ITILE OF INVENTION: SUBFAULT : HIGHER OF SEQUENCES: 44 : CORRESPONDEME ADDRESS: : ADDRESSEE: Townsend and Townsend Khourle and Crev                         | SIREAL: 379 LYCON Avenue CITT: Palo Alto STATE: California COUNTRY: US   | LIFT 94 301 COMPUTER READABLE FORM: COMPUTER: IF LORDY disk COMPUTER: IBM FC COMPATIONS OPERATING SYSTEM: PC-DOS/MS-DOS | SOPTMARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: PULICATION NOMBER: U.S.05(08/201,118 FILING DATE: 22-FEB-1994 CLASSIFICATION: 435 PRIOR APPLICATION DATA:  | APPLICATION WINDER: US 07/864,962 FILING DATE: 09-APR-19/2 ATTORNEY TORDIT THORNATION: NAME: Liebeschuetz, 00. PEGGISTATION WINDER: 37,500.   | TELECOMMUNICATION INFORMATION:<br>  TELEPHONE: (415) 346-240<br>  TELEFAX: (415) 336-342<br>  INFORMATION FOR SEQ ID NO: 4:<br>  SEQUENCE CHARACTRICS:<br>  LEMCTH: 184 hase pairs                                     | TYPE: nucleic acid : STRANDENESS: single : TOPOLOGY: linear : MOLECULE TYPE: CDNA   | Owery Match 59.4%: Score 192: DB 1: Length 1854:<br>Best Local Similarity 100.0%: Pred. No. 2.1e-51;<br>Matches 192: Conservative 0: Mismatches 0: Indels 0: Gaps 0;                  |
|--|---|--|---|--|--|--|---|---|---|--|---|---|
| Cencore version 4.5  Copyright (c) 1993 - 2000 Compugen Ltd.  OM nucleic - nucleic search, using sw model  Run on: April 19, 2002, 08:10:39 ; Search time 130.44 Seconds |   | Scoring table: IDEWITT_NUC<br>Gapop 10.0 , Gapext 1.0<br>Searched: 351203 seqs, 113238999 residues | Total number of hits satisfying chosen parameters: 702406 Minimum DB seq length: 0 Maximum DB seq length: 200000000 | i 8j ∸   | Database: Issued_Patents_NN:*  1: /cgn2_6/ptodta/2/lia/5A_COMB.seq:* 2: /cgn2_6/ptodta/2/lia/5B_COMB.seq:* 3: /cgn2_6/ptodta/2/lia/5B_COMB.seq:* 4: /cgn2_6/ptodta/2/lia/6B_COMB.seq:* 5: /cgn2_6/ptodta/2/lia/RCTUS_COMB.seq:* 6: /cgn2_6/ptodta/2/lia/RCTUS_COMB.seq:* 6: /cgn2_6/ptodata/2/lia/RCTUS_SOMS.seq:* | Pred. No. is the number of results predicted by chance to have a<br>score greater than or equal to the score of the result being printed,<br>and is derived by analysis of the total score distribution. | SUMMARIES Result Query Bo. Score Match Length DB ID Description   | 192 59.4 1854 1 US-08-201-118-4<br>192 59.4 1854 2 US-08-238-821B-4<br>192 59.4 1854 5 PCT-0855-6554-4<br>190.4 58.9 1852 1 US-08-201-118-10<br>190.4 58.9 1852 2 US-08-238-821B-10 | 190.4 58 9 182 5 FCT-6295-65744-10 Sequence 188 8 58.5 1419 2 US-08-194-981E-4 Sequence 188.8 58.5 1591 2 US-06-194-981E-3 Sequence 180.6 55.9 1892 1 US-06-194-981E-3 Sequence 180.6 55.9 1892 2 US-06-218-218-14 Sequence 180.6 55.9 1892 5 US-06-218-218-14 Sequence 180.6 55.9 1892 5 US-06-218-218-14 Sequence | 177.6 55.0 1746 1 05-08-201-118-2<br>177.6 55.0 1746 2 05-08-28-8218-2<br>177.6 55.0 1746 5 PCT-0295-05744-2<br>168 52.0 2009 1 05-08-201-118-6<br>168 52.0 2009 2 05-08-218-818-6<br>168 52.0 2009 5 PCT-0295-05744-6 | 52.0         2258         1 uS-08-201-118-12         Sequence 12           52.0         2258         2 uS-08-218-8218-12         Sequence 12           52.0         2258         5 PCT-0895-05714-12         Sequence 12           47.6         1829         1 uS-08-201-118-8         Sequence 8, sequence 8, sequence 8, sequence 9, sequence 9 | 100.4 31.1 1419 2 US-08-194-981E-2 Sequence 2, 100.4 31.1 1482 2 US-08-194-981E-1 Sequence 1, 91 28.2 8779 2 US-08-750-703-4 Sequence 1, 83.4 25.8 1737 2 US-08-750-703-2 Sequence 2, |

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Ouery Mentch 59.4%; Score 192; DB 2; Length 1854; Best Local Similarity 100.0%; Pred. No. 2.1e-51; Matches 192; Conservative of Hismatches 0; Indels 0; Gaps
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GENERAL INFORMATION:
APPLICANT: GOLDSTEIN, Joyce A. APPLICANT: DE MORNES SEANS, MATJOTIE
APPLICANT: DE MORNES SEANS; MATJOTIE
APPLICANT: DE MORNES SEANS; MATJOTIE A. APPLICANTION: CTYCCHROME P430 219: THE PRINCIPAL SEANS SEQUENCES: G. S-MEPHYNTOIN METABOLISH
NUMBER OF SEQUENCES: G. S-MEPHYNTOIN METABOLISH
CORRESPONDENCE OF S-MEPHYNTOIN METABOLISH
NUMBER OF SEQUENCES: G. S-MEPHYNTOIN METABOLISH
CORRESPONDENCE OF S-MEPHYNTOIN METABOLISH
COMPITE: B100 ALD
CONNETS: THE PLOADE FORM:
CONNETS: THE PROPERATION:
APPLICATION NUMBER: US 08 07 1864, 962
FILLING DATE: C2-FEB-1994
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APPLICANT: GOLDSTEIN, JOYCE A.
APPLICANT: ROMES-SPARKS, MAIJORIE
APPLICANT: ROMES-SPARKS, MAIJORIE
APPLICANT: ROMES-SPARKS, MAIJORIE
APPLICANT: ROMES-SPARKS, MAIJORIE
TITLE OF INVERTION: CLONING, EXPERISON AND DIAGNOSIS OF HURAIN
TITLE OF INVERTION: CLONING: REPRINTANIN METABOLISH
HUMBER OF SEQUENCES: 61
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CLASSIFICATION MAINER: US 00/7201,118
FLILE DATE: 00-748-1992
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Sequence 4, Application US/08238821B
Patent Mo. 5912120
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GENERAL INCOMATION COLOSTEIN, JOYCE A. APPLICANT: GOLDSTEIN, JOYCE A. APPLICANT: GOLDSTEIN, JOYCE A. APPLICANT: GOLDSTEIN, JOYCE A. APPLICANT: GOLDSTEIN, JOYCE A. APPLICANT: GENERS-SPARS, MAI'JOYLE G. APPLICANT: GENERS-SPARS, MAI'JOYLE G. FUNETRON: CLONIAG. EXPRESSION AND DIAGNOSIS OF SUNAN ITILE OF INVENTION: CLONIAG. SOLIS. THE PRINCIPAL DETERMINANT OF STITLE OF INVENTION: TOWNS and and Crew LLP STREET: Two Paracisco Conter, 8th Floor CITY: California CONTESTEI: Two Paracisco CITY: California CONTESTEI: Two Paracisco CITY: California CONTESTEI: Thop Point CONTESTEI: Thop CONTESTEI: Tho
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OTHER INFORMATION: /note- "Corresponds
OTHER INFORMATION: for 65 of Figure 2."
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                 Matches 191; Conservative
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Best Local Similarity 99.54; Pred. No. 6.8e-51;
                                                                                                                          Query match 59.4%; Score 192; DB 5; Length 1854; Best Local Stallarity 100.0%; Prod. Mo. 2.1e-5; Matches 193; Conservative 0; Mismatches 0;
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APPLICART: RORGES-SPARS, MAIOTE APPLICANT: COLOSTEIN, Joyce A.

APPLICART: RORGES-SPARS, MAIOTE APPLICANT: RORGES-SPARS, MAIOTE APPLICANT: RORGES-SPARS, MAIOTE APPLICANT APPLICANT ON THE HUN STREET OF INVERTION: SURFAHILY

MADRIES OF EXPURENCES: 44

ADDRESS PROMERZE APPLICATION: SURFAHILY

COUNTER: 91301

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COUNTER: PAIO ALIO

CONFORTE: US FLORE CALIFORM:

APPLICATION TIPE: Flory dist

CONFORTE: BLORE COMPORTE: PAIOTE NEL CONFORTE: CALIFORM APPLICATION DATA: 22-FRE-1994

CLASSIPICATION DATA: 23-FRE-1994

CLASSIPICATION DATA: 23-FRE-1994

CLASSIPICATION DATA: 23-FRE-1994

ATOMATE: APPLICATION NAME: APPLICATION NAME: Liberschuett, Joe REGISTRATION NAME: Liberschuett, Joe REGISTRATION NAME: 12-FRE-1994

ATOMATE: APPLICATION NAME: 33-505

ATOMATE: APPLICATION NAME: 33-505

ATOMATE: APPLICATION NAME: 13-FRE-1994

ATOMATE : APPL
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1; Indels 0; Gaps

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Ouery Match 58.94; Score 190.4; DB 5; Length 1852; Best Local Similarity 99.34; Pered. No. 68-51; Best Matches 13; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: GUENGERICH, F. PELET
APPLICANT: GUENGERICH, F. PELET
APPLICANT: GUILAW, ELILabbeth H. J.
APPLICANT: GALLAW, ELILabbeth H. J.
ITILE OF INVENTION: BUNNAN
TITLE OF INVENTION: BUNNAN
TITLE OF INVENTION: GUENGERES ON AND PUBLFICATION OF
TITLE OF INVENTION: GUENGERES ON ADDRESSED ON AD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -08-194-981E-4
Sequence 4, Application US/08194981E
Patent No. 5886157
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PCT-US95-05744-10
                                                                                                                                                                                                                                                                                                                                                                                                             Ouery March 58-94: Score 190.4; DB 2; Length 1852: Best Local Similarity 99-34; Pred No. 6.8e-51; Indels 0: Gaps Matches 191; Conservative 0; Mismatches 1; Indels 0: Gaps
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FOTT-01595-05744-10

Sequence 10. Application PC/TUS9505744

Sequence 10. Application PC/TUS9505744

SPELICART: GOLDSTEN, JOYCE A.

APPLICART: GOLDSTEN, JOYCE A.

APPLICART: DE NORES, SOILS MET DE NORES OF TITLE OF INVERTION: CTTCHROME P450 2C19: THE PRINCIPAL TITLE OF INVERTION: CTTCHROME P450 2C19: THE PRINCIPAL TITLE OF INVERTION: OP S-WEPHYNTION WETABOLISM WINDERS DE SEQUENCE. ADDRESS:

CORRESPONDENCE ADDRESS:

ADDRESSONDENCE ADDRESS:

CORPETER: 1391 Lyticon Avenue

STREAT: 319 Lyticon Avenue

CTTT: Palo Alicon Avenue

STREAT: 319 Lyticon Avenue

STREAT: 194301

ADDIUNTIVE: PROPHY GISK

COMPUTER PRADABLE PORH:

MEDIUNTIVE PREADABLE PORH:

COMPUTER: 1849 PC COMPUTED NO.

SOFTWANES: PREADIN PORH:

MAPLICATION MARSH: PCT/US95/05744

FILLING DATE: GO-NAL-1994

PRIOR APPLICATION MARSH: US 08/201,118

FILLING DATE: 27-FEB-1994

FILLING DATE: 37-FEB-1994

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Ouery Match 55.9%; Score 180.6; DB 1; Length 1892; Best Local Similarity 95.3%; Pred. No. 8.7e-48; Indels 0; Gaps Matches 183; Conservative 0; Mismatches 9; Indels 0; Gaps
                                                                                                                                                                                           Onery Match 58.5%; Score 188.8; DB 2; Length 1419; Best Local Similarity 99.0%; Pred. No. 26-50; Matches 199; Conservative 0; Mismatches 2; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                 Sequence 3. Application US/08194981E
PSequence 3. Application US/08194981E
PREMEM INPORMATION:
APPLICANT: GUENCERICL, P. Peter
ITILE OF INVERTION: CTTOCHROWE P450
NUMBER OF SEQUENCES: 68
CORRESSEE: REEDLE 4 ROSENBERG, P.C.
FYREST: SLILE 1200, 127 Peachtree Street, NE
CITY: ALIANA
STATE GOURTE REALABLE FORM:
ADDRESSEE: REEDLE 4 ROSENBERG, P.C.
FYREST: SLILE 1200, 127 Peachtree Street, NE
COMPTRE 13030-1127 Peachtree Street, NE
COMPTRE REALABLE FORM:
ACCUPATION TIPE: Plopy disk
COMPTRE PREALABLE FORM:
ACCUPATION TIPE: Plopy disk
COMPTRE PREALINION RATA:
COMPTRE PREALABLE FORM:
ATTOCHET APPLICATION ROAT:
ATTOCHET APPLICATION NOTA:
ATTOCHET
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Ouery Match 58.51, Score 188.8; DB 2; Length 1591; Best Local Statistity 99.01, Pred. No. 21e-50; Natches 199; Conservative 0; Mismatches 2; Indets 0; Natches 199; Conservative 0; Mismatches 2; Indets 0;

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Matches 183; Conservative
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** WARZYET: Region
LICATION: 1.41

. OTHER INFORMATION: /note- 'Corresponds to positions -41 to-1
75-08-218-5218-511-14

for 2c of Figure 2.**
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0.08-238-8218-14
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: Petent Bo. 5912120
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TYPE: nucleic acid
TYPE: TYPE: Single
TYPE: TINES:
MOLECULE TYPE: DNA (genomic)
HIPPTHETICAL: TES
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 Query Match
 55:91;
 Score 180.6:
 DB 2;
 Length 1892;

 Best Local Similarity
 95.31;
 Pred. No. 8.7e-48;

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GENERAL INTOMALIUM:
APPLICANT: COLDSTEIN JOYCE A.
APPLICANT: COLDSTEIN JOYCE A.
APPLICANT: OCHESTEIN SOUTH MF.
TITLE OF INVENTION: CLOMING, EXPRESSION AND DIAGNOSIS OF HUMAN
TITLE OF INVENTION: CLOMING, EXPRESSION AND DIAGNOSIS OF HUMAN
TITLE OF INVENTION: CLOMING, EXPRESSION AND DIAGNOSIS OF HUMAN
TITLE OF INVENTION: CLOMING, EXPRESSION AND DIAGNOSIS OF HUMAN
TITLE OF INVENTION: CLOMING, EXPRESSION AND DIAGNOSIS.
CONTRESSOURCES.
ADDRESSEE: Townsend and Townsend Khourie and Crev
STREET: 379 LILON Avenue
TITL: PALO ALCO
STATE: California
CONTRES: California
CONTRES: Datentin Release #1.0, Version #1.25
CONTREST ENABLE FORM:
CONTRES PATENTION
MEDIUM TITE: FLOOS/MS-TOS
SOFTWARE: PATENTION NATA:
PRILING DATE: CALANION
PRILING DATE: OCHAY-1994
PRIOR APPLICATION NUMBER: US 08/201,118
FILING DATE: OCHAY-1994
PRIOR APPLICATION NUMBER: US 08/201,118
FILING DATE: OCHAY-1994
PRIOR APPLICATION NUMBER: US 08/201,118
FILING DATE: OCHAY-1994
NAME: DAY-1994
PRIOR APPLICATION NUMBER: 19, 684
REPERENCE CONTRIBUTION:
NAME: DAY MANER: 1994
REPERENCE CONTRIBUTION:
NAME: OCHAY-1994
REPERENCE CONTRIBUTION:
NAME: OCHAY-1994
REPRESENCE CONTRIBUTION:
NAME: OCHAY-1994
REPR
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Februar 20. 5786131

CEREAL INFORMATION:
APPLICART: GOLDSTERH, JOYCE A.
TITLE OF INVERTION: CLONING AND EXPRESSION OF COMPLEMENTARY
TITLE OF INVERTION: SUBFAMILY
TITLE OF INVERTION: SUBFAMILY
MINDRES OF SEQUENCE: 44

CORRESSIONDEAT ADDRESS:
FORMER OF SUBFAMILY
TITLE OF INVERTION: DAYS OF MILTIPLE MEMBERS OF THE HUMAN CTIOC
STREET: PAID ALLO
CORRESTORMED ADDRESS:
TOWNSOR TOWNSOR AND ADDRESS OF THE SUBFAMILY
STREET: PAID ALLO
CORRESTORMED ADDRESS
TOWNSOR TOWNSOR 
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CONFUTER REALCHEE
CONFORTER IN PROCEEDING
CONFORTER IN PROCEEDING
CONFORTER IN PROCEDURE
CONFORTION IN PROCEEDING
SOFTHARE: PRECENTE Release 11.0, Version 11.25
SOFTHARE: PRECENTE RELEASE
FILING DANE: 22.FFB-1994
CLASSIFICATION NAME: 03.094
FILIED DANE: 03.004
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US-08-201-118-2
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RESULT 13

OF 18-218-218-2

Sequence 2. Application US/082388218

Fatest M. S921210

FAREAL HENDRATION

APPLICATT: COLLETEN, Joyce A. APPLICATT: OCHOREFIN, Joyce A. APPLICANT: DE MONES-SPARES, MAIOTIE

TILLE OF INVENTION: CITCENENDE PAGE STATE

CONNESSONDER ADDRESS: TOWNING, EXPENSION AND DIAGNOSIS OF HUMAN

TILLE OF INVENTION: CITCENENDE PAGE STATE

CONNESSONDER ADDRESS OF STATE

CONNESSONDER ADDRESS OF STATE

CONNEST NO MAIOTIE

CONNEST REAL PORTION OF STATE

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CONNEST REAL PROPER STATE

CONNEST REAL PROPER STATE

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APPLICATION MAIORE: US-COS MS - DS

SOSTAWRE: PATENTIN BATA

APPLICATION WARREN: US-COS MS - DS

CLASSIFICATION WARREN: US-COS MS - DS

FILLE DATE

APPLICATION WARREN: 12380-192110US

TELECOMOMICATION HORSEN: 13280-192110US

TELECOMOMICATION INFORMER: 13280-192110US

TELECOMOMICATION INFORMER: 13280-192110US

TELECOMOMICATION INFORMER: 13280-192110US

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9; Indels 0; Gaps
                                                                                                                             best Local Similarity 95.34, Score 177.6; DB 5; Length 1746; Best Local Similarity 95.34, Preed No. 7.5e47; Astches 183; Conservative 0; Hismatches 9; Indels 0;
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Best Local Similarity 92.2%; Pred. No. 8.7e-44;
Matches 177; Conservative 0; Mismatches 15; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oy 127 asgacagagcacactgccctacacagatgctgtgtgcacgaggtccagagataccttg 186 | 11111 | 11111 | 11111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 55.0%: Score 177.6; DB 2; Length 1746; Best Local Similarity 95.3%; Pred. No. 7.5e-47; Matches 183; Couservative 0; Mismatches 9; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATE: GOLDSTEIR, Joyce A. APPLICATE: GOLDSTEIR, Joyce A. APPLICATE: GOLDSTEIR, Joyce A. APPLICATE: GOLDSTEIR, Sonia N.F.

ITILE OF INVESTION: COLOSINA N.F.

ITILE OF INVESTION: CTOCHROME PASO 2C19: THE PRINCI ITILE OF INVESTION: CTOCHROME PASO 2C19: THE PRINCI CHRESCHOLDS ADDRESCES: 61 CORRESCES: 62 STREET: 379 Lytton Avenue CITT: Palo Alto CORPETE STREAM: 979 Lytton Avenue CITT: Palo Alto CONFITE: US CONFITE: 105 CONFITE: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
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GREEKEAL INCOMENTINE, JOYCE A. A. PEDLICARTY GOLDSTEIN, GOLDS
Oy 187 accttctccccaccagcctgccccatgcagtgacctgtgacattaaattcagaaactatc 246
Db 1084 ACCTCATCCCCACCACCTGCCCCATGCAGTGACCTGAGAAATTCAGAAAACTACA
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Search completed: April 19, 2002, 08:10:43 Job time: 2943 sec

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Human cytochrome p
Cytochrome p
Human cytochrome p
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 1
AAD12212 standard; DNA: 8437 BP.
AAD12212:
AAD122212:
AAD12222:
AAD
  Human cytochrome P
Human Cytochrome P
Cytochrome P450 2
Human cytochrome P
Bacterial and mamm
Human cytochrome P
Human cytochrome P
Human cytochrome P
Human derived cyto
Human Lytor cytoch
Human Lytor cytoch
Kammalian cytochrome Cytoch
Kammalian cytochrome Cytoch
                                                                                                                         April 19, 2002, 08:15:28; Search time 277.57 Seconds (without alignments) 997.644 Million cell updates/sec
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313
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        GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                              930621 seqs, 428662619 residues
                                                                                    - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAD12242
AAH51160
AAT11378
AAX14154
AAX19916
AAQ87715
AAT28381
AAT28381
AAT13912
AAX193259
                                                                                                                                                                                                                                                                                             Scoring table: IDEMTITY_NUC
Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score
                                                                                       Of nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Database :
                                                                                                                                                                                                                                                                                                                                                              Searched:
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                                                                                                                            2
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between regions of nucleic acids that were separated by intervening sequence, and also for determining boundaries present in genes containing group 1 type introns such as Tetrahymen TRNA, where self-splicing occurs in the presence of guanosine octotror. The present sequence is human cycochrome P450 (CTP450) 2C19 gene related to the invention.

8\$33333

Sequence 8437 BP; 2392 A; 1501 C; 1541 G; 2654 T; 349 other;

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Determining structure of genes whose sequence is not known from cDNA, by sequencing the gene or gene across exon-intron boundaries using evenly spaced primers comprising nucleic acids that hybridize to the cDNA of gene
                                      /*tag* g //outub_molety* 'Primer' 3258..379 /*tag* h //outub_molety* 'Primer' 3460..3479 /*tag* 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thomann H, Fitzgerald MS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-465380/50.
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The present invention relates to a method for determining gene structure when the general sequencies using method involves sequencing the gene across expointed is minor. The method involves sequencing the gene across expointion boundaries using evenly spaced primers or tiled primers comprises uncleic acids that hybridise to the known coNA sequence of the gene at about 100:300 base intervals and the gene comprises the template. Gene structure can be decrained without the need to sequence the entire gene. The method provides information necessary to determine gene structure and phenotypic gene or fragment. The methods are useful in germline sequence variation analysis. The method is also useful for determining the boundaries Claim 23; Fig 5; 81pp; English.

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                                                                                                                                                                                                                                                                                                                                                 Human; biallelic marker: single nuclectide polymorphism; SNP; MGSTII; microsomal gutathione Stransteress II; malate decarboxylase enzyme; DMEI; MEI; cytochrome P450; glutethione reductase; GSIR; GSIR; GSTS; GIAthir-confaining monoxygenase; FNP; gamma-glutamyltransferase 5; dlepetidase; DP; glucose 6-phosphate dehydrogenase; G6P0B; haplotype; phosphodluconate dehydrogenase; GFDB; dereg*metabolism; phenotype; uridine dlaposphate glucoronosyl transferase; UGT2; asthma; hepatoxicity; ziteuton; ds.
                                Human CYP2CB related DNA containing a biallelic polymorphism SEQ ID 51
Ouery Watch 85.7%: Score 276.8; DB 22; Length 8437; Best Local Similarity 92.9%; Pred. No. 6.4e-79; Andels 1; Gaps Matches 301; Conservative 0; Mismatches 22; Indels 1; Gaps
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Cytochrome P450 2C19; human; liver; PCR; primer; detection; CYP2C19; stereospecific S-mephenytoin 4'-hydroxylase activity; polymorphism; ss.

Homo sapiens.

Cytochrome P450 2C9 clone 25 coding sequence.

Rey Location/Qualifiers
CDS 13..1485
/rtag a // /rtag a

/\*tag- b /note- "Variable position"

Polynucleotides comprising sequences from malate decarboxylase enzyme-related biallelic markers used for genotyping. Claim 13; Page 281; 673pp; English. 

bialitein carkers. The Sequences are treatent to reasons, muser, security control and according accrosomal glutchilone S-transferase II (MSSII), mailate decatorylase enryme (URCINE), cytchrome MSO glutchilone reductase/synthase (GSRSIIS), flatin-choutaining monocygenase (FMO), cytchrome MSO glutchilone reductase/synthase (GSRSIS), flatin-choutaining monocygenases (FMO), comparing a glutcayltransferase S (GGTS), dipeptidase (PD), ducose 6-phosphate diportococyglitransferases (GGTS), dipeptidase (PD), and uridine diportococyglitransferases (GGTS), page according a blailelle carker/polymorphism, which is represented in the biallelic marker polymorphism, which is represented in the biallelic marker polymorphism, which is represented in the biallelic marker polymorphism, which is represented in the matholism. Sequences and degenerate/undefined base. The genes to which the biallelic marker in sequence as a degenerate with the present the general countries of the matholism of the matholism. Sequence and for alternative MSSII caba sequence of the invention in a biological sample for the method is used to determine the frequency in a biological sample of a DME- or MSSIII-talted biallelic marker in a biological sample of a DME- or MSSIII-talted biallelic marker in a biological sample of a DME- or MSSIII-talted biallelic marker in a biological sample of a DME- or MSSIII-talted biallelic marker and to select an individual for inclusion in a clinical trial of a drug createment. The method is also used to detect association between all lelect of an open and plenotype. ne whether an individual suffers or is at risk of developi or is at risk of developing hepatoxicity on treatment with

Sequence 1001 BP; 270 A; 166 C; 178 G; 384 T; 3 other;

242 ctatotoattocoaaggtaagtttgtttetoctacactgcaactccatgttttcgaagtc 301 437 ctacctcatccccaaggtaagcttgtttctcttacactatatttctqtacttctqaaatt 496 bear March 69.01: Score 223; DB 21: Length 1001; Beat Local Similarity 83.01; Pred. No. 5.18-62; Matches 253; Conservative 1; Mismatches 51; Indels 0: 302 ccana 306 සි පි 8 6 8 Š 8 5 8 888

497 tccaw 501

AAT11378 standard; cDNA; 1854 RESULT 3 AAT11378 1D AAT13 XX AAT13 XX AAT13 XX 09-SI

09-SEP-1996 (first entry) AAT11378;

1-concoding regions but contained 2 single base changes at positions (197) and (142). One of these base changes as conservative but the other (197) and (142). One of these base changes as conservative but the other clones 29c and 60 buffer by one nucleotide in the coding region.

Clones 29c and 60 buffer by one nucleotide in the coding region.

Clones 29c and 60 buffer by one nucleotide in the coding region.

Clones 29c and 60 buffer by one nucleotide in the coding region on solution is signal 21 bases from the poly A tail. One 60 buffer an unusually long 3'-noncoding region containing three possible containing three possible containing three possible containing three possible and a polyadenylation signals with no poly A tail. The differences in the 3' concoding regions could represent alternate splicing, allelic containing three possible coding regions could represent alternate splicing, allelic containing three coding regions the streams are more and a coding region. They are most smill three coding region they are most smill to 209 (82% amino acid homology) Of the 50 clones encoding 209, only two allelic variants were of the 209 clones were identical with clone 65, and 11 were 10 oith clone 25. Clones 25 and 65 are identical in the 5' and New isolated cytochrome P450 2C subfamily member identifying drugs metabolised by S-mephenytoin 4' activity and to develop other screening assays De Morais SMF, Goldstein JA, Romkes-Sparks M; (USSH ) US DEPT HEALTH & HUMAN SERVICES. Example 2; Page 95-96; 169pp; English. 08-MAY-1995; 95WO-US05744. 06-MAY-1994; 94US-0238B21. WPI; 1996-077257/08. P-PSDB; AAR89862. W09530766-A1. 16-NOV-1995. 

Sequence 1854 BP; 513 A; 424 C; 381 G; 536 T; 0 other;

Query Match 59.4%; Score 192; DB.17; Length 1854; Best Local Similarity 100.0%; Pred. No. 7.3e-52; Indels 0; Gaps Matches 122; Conservative 0; Hismatches 0; Indels 0; Gaps

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1031 magacaggagccacatgccctacacagatgctgtggtgcacgaggtccagagataccttg 1090

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The present sequence encodes a fusion proteins comprising a portion of a abacterial organization of a mammalian cytochrome P450 protein and also a portion of a mammalian cytochrome P450 protein. The fusion protein can oxidise hydrocarbons or any compound having a carbon-hydrogen bond. The fusion protein can be used for hydroxylating a compound to be oxidised. It can also be used in the bioremediation of an environmental pollutant. Since the fusion the bioremediation of an environmental pollutant. Since the fusion protein is soluble, it can be subject to structural elucidation by X-ray expressed in soil bacteria to facilitate bioremediation.
Bacterial and mammalian chimeric cytochrome P450 protein encoding DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New P450 fusion proteins - comprising a portion of a bacterial cytochrome P450 protein and a portion of a mammalian cytochrome P450 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacterial; mammalian; cytochrome P450; chimeric; fusion protein; oxidise; hydrocarbon; carbon-hydrogen bond; hydroxylating; bioremediation; environmental pollutant; ss.
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                                                                                                                                                                                                                                                                                                                                                                 AAX19916 standard; DNA; 1356 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-AUG-1998; 98WO-US16979.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-JUN-1999 (first entry)
                                                                                                                                                  (UYRP ) UNIV ROCHESTER.
                                                                                               247 tcattcccaagg 258
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P-PSDB; AAY04126.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            AAX19916;
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MAX199
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                                        Oy 187 accticicccaccacagcigcccatgoagtgacctgtgacattaaatcagaaactaic 246

Db 1091 accticicccaccagcagccgccaggaggacctgrgacattaaattcagaaactai 1150

Db 1091 accticicccaccagagcgcccatgaaggacctgrgacattaaattcagaaactai 1150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cochrome P450; drug screening; S-mephenytoin 4'-hydroxylase;
identification; autagenic; carringenic; cytotoxic; haemoprotein;
xenobiotic; environmental poliutani; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human cytochrome P450 2C9 clone 25 cDNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAV44154 standard; cDNA; 1854 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Goldstein JA, Romkes-sparks M;
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09-APR-1992; 92US-0864962.
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                                                                                                                                                                                               WPI; 1998-436528/37.
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ANV41154
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Oucry Match 58.9; Score 190.4; DB 20; Length 1356; Best Local Similarity 99.38; Pred. No. 2.18-51; Matches 191; conservative 0; Mismatches 1; Indels 0; Gaps Sequence 1356 BP; 349 A; 386 C; 323 G; 298 T; 0 other; 8 3 8 Š

8 8 5

Ouery Match 59.4%; Score 122; DB 19; Length 1854; Best Local Similarity 100.0%; Pred. No. 7.38-75. Indels 0; Matches 192; Conservative 0; Mismatches 0; Indels 0; Gaps

Sequence 1854 BP; 513 A; 424 C; 381 G; 536 T; 0 other;

187 accticicccaccagectgecccatgeagtgacctgtgacattaaatteagaaactate 246

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Human cytochrome P450; amplification; PCR; primer; expression vector;
yeast MaDPH-1450 reductase; asfety; fusion protein; metabolite;
cartinogen; mitugen; liver metabolism; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Evaluation of safety of a chemical cpd. - using recombinant yeast expressing human cytochrome p450 and a yeast NADPH-P450 reductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bayashi K, Kaneko H, Komai K, Nakatsuka I, Sakaki T;
Yabusaki I;
                                                                                                                                                                                                                                                                                                                                                                                              Human cytochrome P450 molecular species 2C9 cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Examples; Page 23-25; 124pp; English.
                                                                                                                                                                                                                    AAQ87715 standard; cDNA; 1473
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(SUMD ) SUMITOMO CHEM CO LID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-JUL-1993; 93JP-0180246.
20-JUL-1993; 93JP-0201120.
30-JUL-1993; 93JP-0208279.
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                                                                                                                                                                                                                                                                                                                                        10-MOV-1995 (first entry)
                                                          Db 1022 tcattcccaagg 1033
247 tcattcccaagg 258
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P-PSDB; AAR72361.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-JUL-1994;
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                                                                                                                                                                                                                                                                              AAQ87715;
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The nucleotide sequence of the CDNA encoding the human cytochrome P450

St species 2C9. The gene encodes a protein of 491 amino acids. The CDNA

vas amplified by PCR using the primers AA087735-8. The product was

Cloned into the yeast expression vectors PAM316 or PAMRR to produce the

vervors p209 for the expression of the cytochrome P450 alone or p209R

Compound by reacting the chemical compound with recombinantly produced

The vectors are used in a method for evaluating the safety of a chemical

Compound by reacting the chemical compound with recombinantly produced

CAA0877189 or 3M (AA087717), or their auxiliary species and variants

CAA0877189 or 3M (AA087777), or their auxiliary species and variants

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Sequence 1473 BP; 413 A; 345 C; 319 G; 396 T; 0 other;

Opery Match 58.9%; Score 190.4; DB 16; Length 1473; Best Local Similarity 99.5%; Pred. No. 2.2e-51; Matches 191; Conservative 0; Mismatches 1; Indels 0; Gaps Š

Human cytochrome P450: amplified; PCR: polymerase chain reaction; primer; lufuer; yeast; expression vector; NADBH-P450 reductase; ADH gene promoter; evaluation; safety; fusion protein; metabolite; detoxification; carcinogenic; ds. 197 accttctcccaccagcctgcccatgcagtgacctgtgacattaaattcagaaactatc 246
1079 accttctcccaccagcctgcccatgagtgacctgtgacattaaattcagaaactatc 1138 Nevel method for the evaluation of the safety of a cpd. - using a human ortochrome P405 and yast NADBH reductes to determine whether the analyte opf. is detoxified or metabolised to a cartinogen Ruman cytochrome P450 molecular species 2C9 gene. Example 1; Page 20-22; 74pp; Japanese. AAT28381 standard; DNA; 1473 (SUMO ) SUMITOMO CHEM CO LTD. 17-JUN-1994; 94.JP-0136053. 20-JUL-1993; 93.JP-0201120. 30-JUL-1993; 93.JP-0208279. 15-JUL-1994; 94JP-0164184. 11-OCT-1996 (first entry) WPI; 1996-182311/19. P-PSDB; AAR93168. Homo sapiens. JP08056695-A. 05-MAR-1996. AAT28381; AM728381

AM728381

AM728381

AM728381

AM728381

AM728381

AM72

AM728381

This is the nucleotide sequence of the human cytochrome P450 molecular species 209 gene which encodes a protein of 490 anino acids. The gene sequences a protein of 490 anino acids. The gene of 9.0 and 9.0 a 9%; Score 190.4; DB 17; Length 1473; 5%; Pred. No. 2.2e-51; 0; Mismatches 1; Indels 0; Ouery Match 58.9 Best Local Similarity 99.5 Matches 191; Conservative

1; Indels 0; Gaps

an sa Maria. Magazilan dalah mendah sabatan bebagai beragai beragai beragai beragai beragai beragai beragai beragai beragai

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us-09-763-292-3.rng
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Homo saplens.
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                                                                                  Buman derived cytochrome; P4502C9; commercial cDNA library; yeast; itemafection; recombinant production; expression vector; mammal; itemanistation; ensistiation; annual; operators reactive; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence encodes the human derived cytochrome (HDC) P45029, which was obtd. from a commercial cDNA library. Teast were transfected with an expression vector contg, the HDC cDNA cultured and then disrupted to dive a nicrosomal fraction. The EDC was purified from the fraction, and used to lammulse and sensities a mammal. Blood was drawn from the mammal, and an anti-HDC antibody solated. The antibody obtd. recognises HDC P405029, partic. at a serum dilution rate of 1:10000, and is substantially without cross reaction to other HDC P450 spp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Autibody recognising human derived cytochrome P4502C9 - allows apecific detection of cytochrome P450 species in humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1473 BP; 413 A; 345 C; 319 G; 396 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Pages 11-13; 13pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Busan derived cytochrome P4502C9 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAT17404 standard; cDNA: 1473 BP.
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P-PSDB; AAR81465.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-JAM-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAT17404;
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Ouery Match 58.9%. Score 190.4; DB 11; Length 1918; Best Local Smallarity 99.5%, Pred. No. 2.4e-51; Indels 0; Gaps Matches 191; Conservative 0; Mismatches 1; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The P-450 produced from plasmid phPA6 in a yeast expression system preferably Socriaromyces AM12, can be used for treat human liver disorders, oxidising various chemical substances.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Recombinant plasmid, for yeast for liver treatment .
comprises human liver cytochrome P-450MP gene obtd. from yeast,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1818 BP; 516 A; 412 C; 376 G; 514 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                           Human liver cytochrome P-450 encoding gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-450; cytochrome; Saccharomyces cerevisiae;
liver disorders; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
1..1443
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure: Fig 4; 9pp; Japanese.
                                                                                                                                                                                                                                                                AAQ03599 standard; DNA; 1818 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (AGEN ) AGENCY OF IND SCI TECH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-SEP-1988; 88JP-0225955.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-SEP-1988; 88JP-0225955.
                                                                                                                                                                                                                                                                                                                                                               03-SEP-1990 (first entry)
                                                                                              WPI; 1990-121045/16.
P-PSDB; AAR04043.
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127 aagacaggagccacatgcctacacagatgctgtgtgtgcacgaggtccagagataccttg 186

Ower Watch 58.94. Score 190.4. DB 17; Length 1473; Best Local Smallarity 95.54, prof. No. 2.2e-51; Indels 0: Gaps Matches 191; Conservative 0: Mismatches 1: Indels 0: Gaps

1029 aagacaggagccacatgccctacacagatgctgtggtgcacgaggtccagagatacattg 1088

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ร์การเลย พ.ศ.ค. (เพิ่มพิธีสัญษาสหรับ ซึ่ง พ.ศ.ย

Cytochrome P450 2C19; human; liver; PCR; primer; detection; CYP2C19; stereospecific S-mephenytoin 4'-hydroxylase activity; polymorphism; &

Location/Qualifiers 11..1483

Homo sapiens.

Cytochrome P450 2C9 clone 65 coding sequence.

09-SEP-1996 (first entry)

AAT11381;

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RESULT 11
AAT11381
ID AAT11381 standard; CDNA; 1852 BP.
XX
                                                                                                                         The present invention describes a fusion proteins comprising a portion of a bacterial cytochrome P400 protein and also a portion of a mammalian cytochrome P400 protein and also a portion of a mammalian cytochrome P400 protein. The fusion protein can oxidise hydrocarbons or any compound having a carbon-hydrogen boad. The fusion protein can be used for hydroxylating a compound to be oxidised. It can also be used in the bloremediation of an environmental pollutent. Since the fusion protein is anoluble, it can be subject to structural elucidation by X-ray expressed in soil bacteria to facilitate bioremediation. The present sequence encodes amamalian cytochrome P400 protein CTP2C9 from the present invention.
                                 Amgacaggagccacatgccctacacagatgctgtggtgcacgaggtccagagatacattg 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New P450 fusion proteins - comprising a portion of a bacterial cytochrome P450 protein and a portion of a mammalian cytochrome P450 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacterial; mammallan: cytochrome P450; chimeric; fusion protein; Oxidise; hydrocarbon; carbon-hydrogen boad; hydroxylating; birr=mediation; environmental pollutant; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1845 BP; 507 A; 424 C; 380 G; 534 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                          Manmalian cytochrome P450 protein CYP2C9 encoding DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure, Page 10-11; 51pp; English.
                                                                                                                                                                                                                                                                   AAX19925 standard; DNA; 1845 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-AUG-1998; 98WO-US16979.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-AGG-1997; 97US-0056754.
                                                                                                                                                                                                                                                                                                                                                   11-JUM-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UYRP ) UNIV ROCHESTER.
                                                                                                                    Jones JP, Shimoji M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-190131/16.
P-PSDB; AAI04127.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W09908812-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Manmalia.
                                                                                                                                                                                                                                                                                                          AAX19925;
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MAX
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The sequences given in AAT11378-81 encode allelic variants of cytochrome 78.0 CF. The following control of clones isolated for 1209.

78 10 CF. The majority of clones isolated for 1209.

70 If the 50 clones encoding 209, only two allelic variants were found.

70 of the 209 clones were identical with clone 50, and il were ledentical 39 control of 100 clones were identical with clone 55, and 140 clone 57.

71 choncoding regions but contained 2 single base changes at positions control of 1075 and 1405. One of these base changes was conservative but the other results in one amino acid difference at position 359, ille to Leu. The clones 20c and 60 differ by one nuclectide in the coding region of control of 154, which results in a single amino acid change. This to Met at position 355. Clone 20c has a very long, 198 bp. 5° noncoding region containing three position 60 clones ignal 21 bases from the poly A tail. Clone 6b has an unusually long 3° noncoding region containing three possible conformation signals with no poly A tail. The differences in the 3° non-coding regions could represent alternate splicing, allelic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated cytochrone P450 2c subfamily member - used for identifying drugs metabolised by 5-mephenytoin 4'-hydroxylase activity and to develop other screening assays
. /*tag= a
product- Cytochrome P450 C9 clone 25
misc_difference 71085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              De Morais SMF, Goldstein JA, Romkes-Sparks
                                                                                                              /*tag= b
/note= "Variable position"
                                                                                                                                                                                                                                       /*tag- c
/note- "Variable position"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 2; Page 104; 169pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-MAY-1995; 95WO-US05744.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-MAY-1994; 94US-0238821.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1996-077257/08.
P-PSDB; AAR89865.
                                                                                                                                                                                                      misc_difference
                                                                                                                                                                                                                                                                                                                                                                 W09530766-A1.
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Ouery Match 58.9%; Score 190.4; DB 20; Length 1845; Best Local Similarity 99.5%; Pred. No. 2.4e-51; Matches 191; Conservative 0; Mismatches 1; Indels 0; Gaps

127 asgacajascacatgcctacacagatgctgtggtgcacagagtccagagataccttg 186

endobiotics such as steroids, fatty acids and prostaglandins.

Sequence 1852 BP; 514 A; 424 C; 380 G; 534 T; 0 other;

0 **x** 00

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Mon Apr 22 08:41:46 2002
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cc variants, or possibly separate genes. These clones are designated as callelive variants of ZGB because they differ by only one base in the coding region. They are most similar to 209 (82% maino acid homology).

XX and 2019 (81% maino acid homology).

XX squence 1852 BP: 514 A; 424 C; 380 G; 534 T; 0 other;
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Ouery Match 58.9%; Score 190.4; DB 17; Length 1852; Best Local Similarity 99.5%; Pred. No. 2.4e-51; Matches :191; Conservative 0; Mismatches 1; Indels 0; Gaps 

Human cytochrome P450 2C9 clone 65 cDNA AAV44157 standard; cDNA; 1852 BP 06-0CT-1998 (first entry) AAV44157;

Cytochtrame P450; drug screening; S-mephenytoin 4'-hydroxylass:: identification, mutapenic; carcinogenic; cytotoxic; haemoprotein; remobiotic; environmental poliutant; ss.

Home sapiens.

28-JUL-1998. US5786191-A.

22-PEB-1994; 94US-0201118.

22-PEGB-1994; 94US-0201118. 09-APR-1992; 92US-0864962.

(GOLD/) GOLDSTEIN J A. (ROML/) ROMKES-SPARKS M.

Goldstein JA, Romkes-sparks M;

WPI; 1998-436528/37.

Screening for drugs metabolised by cytochrome P450 - for identifying mutagenic, carcinogenic, or cytotoxic compounds

Example 2; Column 53-56; 63pp; English.

This sequence encodes a human cytochrome P450 2C9 polypeptide isolated from clone 65. This polypeptide is used in a method to screen for a drug that is metabolised by a cytochrome P450 having S-mephenytoin 4'-hydroxylase extivity. The protein can also be used to identify a mategapaic, carcinogenic or cytochac compound. Cytochrome P450 are a large family of hemosprotein enzymes capable of metabolising xenoblotics such as drugs carcinogens and environmental pollutants as well as

Human: biallelic marker: single nucleotide polymorphism: SNP: MGSTII; microsomal glutathione Stransferase II; maltet decroboxylase enzyme; DMEI; MEI; cytochrome P160; glutathione reductase: GSHR: GSHS: GGT5; directaining monocoxygenase: FMO; gamma-glutam/transferase 5: dipeptidase: DP; glutose 6-phosphate debydrogenase: GGPBI: haplotype: uridine diphosphate glucoronate dehydrogenase: MCBI: dipeptidase: DP; glucose 6-phosphate dehydrogenase: GGPBI: haplotype: uridine diphosphate glucoronosyi transferase; UGT2; asthma; hepatoxicity; illeuton: ds. Ruman CYP2CB related DNA containing a biallelic polymorphism SEQ ID 53. Onery Match 58.9%; Score 190.4; DB 19; Length 1852; Best Local Similarity 99.3%; Pred. No. 2.4e-51; Matches 191; Conservative 0; Mismatches 1; Indels 0; Gaps à à a Oy D

Sequences AM51110-AM31193 represent human DNA fragments which contain balallelie markers. The sequences are related to various human genes including microscanal glutathione 5-transferase II (MGSTI1), malate decarboxylase enzyme (DMEI/MEI), cytochrome P450, glutathione p460, edutathione genes genes graph graphase (GSMEI/MEI), cytochrome p450, glutathione p450, glutathione p450, glutathione p450, glutathione p450, glutathione p450, glutathione gamma-glutamyltransferase 5 (GGTS), dipeptidase (DP), glutose 6-phosphate Polynucleotides comprising sequences from malate decarboxylase enzyme-related biallelic markers used for genotyping . Blumenfeld M, Bougueleret L, Chumakov I, Cohen-Akenine A; Claim 13; Page 283; 673pp; English.

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Mon Apr 22 08:41:46 2002
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debydrogenase (G6DBL), phosphogluconate dehydrogenase (PGDB), and uridine diphosphate glucoronosyl transferases (UGT2). Each of these sequences contains a biallelic marker/polymorphism, which is represented in the sequence as a degementate/undefined base. The genes to which the bialloic marker containing sequences are related are involved in drug metabolism. Sequences AMB15184 - AMB15189 represent the qenomic sequence of the fact of the fact of the septiment of the sequence of the marker containing sequences are related are involved in drug metabolism. Sequences AMB15184 - AMB15189 represent the qenomic sequence of the metabolism command of the sequence of the set of the amplification of human genomic DNA sequences. AMB1980 and AMB1809 of the used to make used in a molecular a method of genotyping comprising determining the involution of marker in a biological sample. The method is used to determine the frequency in computation of an allele of a DNE or MOST-II related biallelic marker and to select an individual for inclusion in a clinical trial of a drug content of the section of the section between haplotype and phenotype.

Createment The method is also used to detect association between haplotype and phenotype or allele specific amplification assays. Sequencing assays or allele specific amplification assays. The method casted to select an individual suffers or is at risk of developing negation.
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Purifying recombinant cytochrome P450 · by utilising novel combinations of detergents and enzyme inhibitors

Disclosure; Column 55-56; 91pp; English.

Gillam EMJ, Guengerich FP, Guo Z, Sandhu

(UYVA-) UNIV VANDERBILT.

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Cytochrome P450; detergent; enzyme inhibitor; non-ionic; ionic; purification; drug oxidation; steroid; carcinogen; pesticide; human: ss.
                                                                                                                                                                                                                 Ouery Match 58.5%; Score 189; DB 21; Length 1001;
Best Local Similarity 93.3%; Pred. No. 5.1e-51;
Matches 251; Conservative 0; Mismatches 9; Indels 9; Gaps
                                                                                                                                                                                                                                                                                                                                                    Sequence 1001 BP; 251 A; 180 C; 193 G; 366 T; 11 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human cytochrome P450 2C10 variant DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAI22716 standard; DNA; 1419 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94US-0194981.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US5436157-A.
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This invention describes a recombinant cytochrome P450 protein which is purified from a host cell culture using a combination of detergents and enzyme inhibitors. The method comprises (a) fractionating the host cells to prepare their membranes, (b) adding a non-ionic detergent to the membranes, (b) adding a non-ionic detergent to the membranes in a concentration of 0.8 % to 2% (w/v) in a cetergent to the membranes in a concentration of 0.8 % to 2% (w/v) in a detergent to the membranes in a concentration of 0.4% to 0.8% (w/v) in a cetergent to the membranes in a concentration of 0.4% to 0.8% (w/v) in a purifying the protein ratio of between 2:1 to 4:1 (d) centrifying the protein through a diethylaminoethyl-beaded column, then through a carboxymethyl-beaded column, and finally through a carboxymethyl-beaded particles. The method simplifies the carboxymethor of P450 proteins which are responsable for catalyshing the oxidation of P450 proteins, by the use of improved expression vectors and novel detergent combinations.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cytochrome P450; detergent; enzyme inhibitor; non-ionic; ionic; purification; drug oxidation; steroid; carcinogen; pesticide; human; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 58.51; Score 188 B. DB 20; Length 1419; Best Local Similarity 99.04; Pred. No. 6.9e-51; Indels 0; Gaps Matches 190; Conservative 0; Mismatches 2; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1419 BP; 409 A; 332 C; 307 G; 371 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human cytochrome P450 2C10 DNA.
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10-FEB-1994; 94US-0194981
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(UTVA-) UNIV VANDERBILT.

Gillam EMJ, Guengerich FP, Guo Z, Sandhu P;

WPI; 1999-228609/19.

Purifying recombinant cytochrome P450 · by utilising novel combinations of detergents and enzyme inhibitors

Disclosure; Column 53-54; 91pp; English.

This invention describes a recombinant cytochrome P450 protein which is purified from a host cell culture using a combination of detergents and engrge inhibitors. The method comprises (a) fractionating the host cells to prepare their membranes, (b) adding a non-ionic detergent to the membranes, (b) adding a non-ionic detergent to the membranes in a concentration of 0.8% to 2% (w/w) in a cetergent introduce in a concentration of 0.8% to 2% (w/w) in a cetergent protein ratio of between 4:1 to 10:1, (c) adding an ionic detergent protein ratio of between 2:1 to 4:1 (d) centrifuging the membrane-detergent mixture to remove insoluble materials and (e) purify trying the protein through a deterphalmicochyl-beaded column, then culturing the protein through a deterpentyl-beaded column, and finally through as chiptorylapatite column, the method is used to purify cyclochrome P450 cortection, which are responsible for catalysing the oxidation of e450 certains, which are responsible for catalysing the oxidation of e450 proteins, by the use of improved expression vectors and novel detergent combinations.

Sequence 1591 BP; 443 A; 372 C; 353 G; 423 T; 0 other;

Owery Match 58.5%; Score 188.8; DB 20; Length 1591; PBest Local Similarity 99.0%; Pred. Mo. 77.3e-51; Indels 0; Gaps Matches 190; Conservative 0; Mismatches 2; Indels 0; Gaps

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|---|--|---|--|--|--|--|--|---|---|---|---|--|---|--|--|---|---|---------------------|--|--|---|--|
| 4.5<br>Compugen Ltd.  |  | Search time 2723.34 Seconds (without alignments) 1274.496 Million cell updates/sec  | aaattcatagtatcatttt 323  |  | dues   | rs: 22703874   |  |   |   |   |   |  |   |  |  | cted by chance to have a of the result being printed, score distribution.   |   | Description         | AV58443 AV58443<br>AV558435 AV658435<br>AV646130 AV646130<br>AV646130 AV646130 | BG567504 602586239<br>BG186520 RST5487 A | BG205598 RST25061<br>BG205076 RST24495<br>BG198889 RST18160 | BG184407 RST3332 A<br>AV651261 AV651261<br>AV652420 AV652420                                   |
| GenCore version 4.5<br>Copyright (c) 1993 - 2000 Con  | nucleic search, using sw model   | April 19, 2002, 08:07:49 ; Sear   | US-09-763-292-3<br>323<br>1 ccctgaattgctacaacaa  | IDENTITY_NUC<br>Gapop 10.0 , Gapext 1.0  | 11351937 seqs, 5372889281 residues   | of hits satisfying chosen parameter                      | Minimum DB seq length: 0<br>Maximum DB seq length: 200000000                         | Post-processing: Minimum Match 0%<br>Maximum Match 100%<br>Listing first 45 summaries | EST:*<br>1: em_estfun:*<br>2: em_esthum:* | 1: eng_estin: * 4: eng_estin: * 5: eng_estin: * 6: eng_estin: * 7: eng_estin: * |   | 11: gb_est2:*<br>12: gb_htc:*<br>13: gb_gss:*<br>14: granges   |   |  | 21: en gss_other:*   | Pred. No. is the number of results predicted by chance to have a<br>recover greater than or equal to the score of the result being printed<br>and is derived by analysis of the total score distribution. | SURMARIES   | Watch Length DB     | 58.9 599<br>58.9 603<br>58.9 614   | 58.9 819 11<br>58.9 856 11               | 58.9 901 11<br>58.9 907 11<br>. 58.9 909 11                 | 58.5 388 11<br>58.5 620 10<br>58.5 661 10  |
| •   | OM nucleic - nuc   | Rub on:   | Title:<br>Perfect score:<br>Sequence:  | Scoring table:   | Searched:  | Total number of  | Minimum DB seq<br>Maximum DB seq   | Post-processing   | Database :                                | a .   | - |  |   |  |  | Pred. Mo.<br>score gre<br>and is de   | *   | Kesuit<br>Bo. Score | 7.2 190.4<br>3 190.4   | 5 190.4                                  |   | 10 188.6.<br>11 198.8<br>12 188.8  |

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Mydefilion Girghelia

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Human.

ISA Homo sapiens

Briaryota. Fetzoe: Chordata: Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria: Primates; Catarrinii; Hominidae; Homo. Sapiens

Rearyota. Full. R. Peng, Y. Liu, F. Ou, J. Song, H., Cheng, I., Ou, J. Song, H., Cheng, I., Ou, J., Song, H., Chen, I., Ou, J., Shanghai

Chinese National Human Genome Center at Shanghai

Si Guo Shaujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai

Jogo, P. R. Chine, Chen, 
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PRIATYOLE : Metacoa; Chordata; Craniata; Vertebrata; Euteleostomi; Marmalia; Eutheria; Petacoa; Chordata; Craniata; Vertebrata; Euteleostomi; Marmalia; Eutheria; Primates; Catarrinni; Homindae; Homo.

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RS 'Mu'X. 'LiN 'Peng'Y. 'LiNe', Cang'B.', Cheng'Z.', Ou'J.', Eng'J.', Xu'S.', Ciw, Yu'Y. 'Lin', Chen'Z.' and Han'Z.', Song H.', Cheng'Z.', Ou'J.', Eegy, L.', Xu'S.', Ciw, Yu'Y. 'Lin', Jia', Du'J.', Frigor. 'Bong apiens cDM, Cine (bu'N', Tu'Y. 'Jia', Du'J.', Frigor. 'Bong apiens cDM, Cine (bu'N', Cine 
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Oy 67 cagetaaagtccaggaaggattgaacgtgtgattggcagaaaccggagcccctgcatgc 126
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175487 Athersys RAGE Library Homo sapiens CDNA, mRNA sequence.
186520.1 GI:13708207
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Best Local Similarity 99.5%: Pred. No. 5.1e-41;
Matches 191; Conservative 0; Mismatches 1; Indels 0; Gaps
mRNA sequence.
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BG567504.1 GI:13575157
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ENMANGES WAS A CANDIAGE. CATAININI: Hominidae: Homo.
NAMMADIA: Louberia: Primates: Catarrhini: Hominidae: Homo.
12. (Dasses I to 907)
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14. Sherf, B. Neudlett, S., Jackson, P. D., Perry, R.,
15. Harrington, J., Sherf, B., Rumchardran, R., Whittington, J.,
16-renr, L., Krashoc, D., Welligott, K., Clark, S., Mays, R., Smith, E.,
veloso, N., Hess, J., Cothren, K., Lo, K., Offenbacher, J., Danzig, J.
and Ducar, M. Concert, Genome-vide Protein Expression Libraries using Random
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And Local Scott J. Cain
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Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression Nat. Biotechnol. 19 (5). 440 (2001) In press Contact: SCOLT J. Call
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71 9900
71 9596
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3101 Carnegle Ave, Cleveland, OH 44115,
Tel: 216 431 9900
Eax: 216 384 5956
Eaxi: 15 calnethersys.com
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Explaints. Metacas: Chordata; Craniata; Vertebrata; Enteleostomi; Medarayote; Metacas; Chordata; Craniata; Vertebrata; Enteleostomi; Homos sapiens

Explaints. Eutheria: Primates; Catarthini; Hominidae; Homeo.

Explaints. Piberf. B. Fundlett. S., Jackson, P. D., Perry, R. Barrington, J. J., Sherf. B. Rundlett. S., Jackson, P. D., Perry, R. Barrington, J. Cohnen, K. Messaboc, D. Welligott, R., Clark, S., Mays, R. Smith, E. Veloso, W. Hess, J. Cohnen, K. Jo, K., Offenbacher, J., Danzig, J. Carlaton of Gene Expression Libraries using Random AL Mat. Biotechnol. 19 (5), 440 (2001) in press

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                     gh quality sequence stop: 354.

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| Best Local Similarity 99.0%; Pred. No. 1.3e-40;<br>Matches 190; Conservative 0; Mismatches 2; Indels 0; Gaps 0;   | Oy 187 acctroccoaccagoctgoccotgoagtgacctgtgacattaaattcagaaactatc 246  |
|---|---|
| 67 cayctaaagtccaggaagagattgaacgtgtgattggcagaaaccggagccctgcatgc 126<br>  | 247 tcattccaagg 258 [11]  |
| 127 asgacaggagcocatocctacacagatgttgtgtgtgcacgaggtccagagataccttg 186 11111111111111111111111111111111111   | SULT 12   |
| 187 accttctccccaccagctgcccatgcagtgactgtgacattaaattcagaactatc 246  | APOSATA<br>LOCUS AV652420 661 bp mRNA EST 07-SEP-2000<br>DEFINITION AV652420 GLC Homo sapiens cDNA clone GLCDAB09 3', mRNA sequence.<br>ACCESSION NV65240 ACCESSION AV65240 ACCESSION A |
| 247 tcattcccasgg 258  | VENDOR KONSTAULT GLISOLANSA<br>SOURCE Dimman. ORGANISH Homo sapiens   |
| FILE 113  | Eukaryota: Metazoa; Chordata: Craniata: Vertebrata: Euteleostomi;<br>Mamalia: Eutheria: Primates: Catarrhini; Hominidae: Homo.<br>REFERENCE 1 (bases 1 to 661)  |
|   | AUTHORS Glan.B. W.T., Huanglo. Huanglo. Kangp B., Gaox.x., Xuz.Y. Xiao.H., Xu.X., Li.M. Peng.X., Liu.F., Ou.J., Song.H., Cheng.Z., Ou.J., Zeng.L., Xx.S., Gu.Y., Tu.Y., Jia.J., Fu.G., Ren.S., Zhong.M., Lu Zeng.L., Year, Y., Chen.Y., And Han.? Fu.G., Ren.S., Zhong.M., Lu   |
| XXXX510M AV51241. AV51241.1 GI:9872275 FYFWPORS EST. MARGA. MARGA. MARGA.   | 11TLF Homo saplens CDMA clone JOURNAL Unpublished (200) COMMENT Contact: Regard Han   |
| _   | Chinese National Human Genome Center at Shanghal<br>351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghal<br>201203, P. R. China   |
| AUTHORS Qian, W. V., Ruang, Q., Huang, C., Kang, B., Gao, X., Xu, Z., Xiao, H., AUTHORS Qian, W. X., X., Li, M., Pener, Y., Liu, F., Ou, J., Sonq, B., Cheng, Z., Qu, J., | Tet: 86-21-50801919(ex.4>)<br>Fax: 86-21-50801922 (<br>Email: hansg@chgc.sh.cn  |
|   | This clone is available at CHGC in Shanghai. FEATURES Location/Qualifiers   |
| JOGNAL, Unpublished (2000) JOGNAL, Unpublished (2000) Contact Contact (2000)  | source 1oou / Organism*Homo sapiens* / Organism*Homo sapiens* / / / / / / / / / / / / / / / / / / /   |
|   | /clone="GLCDAB09"<br>/clone_lib="GLC"<br>//ice: type="GLC"  |
| 201203.1 P. R. China<br>Tel: 66-21-50801919(ex.45)<br>Par: 66-21-50801922   | /deb.stage="Adult" /deb.stage="A          |
| <pre>Parall: hazagetoc.sh.co<br/>This clone is available at CRCC in Shanghai.<br/>Location/Qualifiers</pre>   | BASE COUNT 166 a 189 c 130 g 175 t 1 others   |
| /organism="Homo sapiens"<br>/db_xref="taxon:9606"<br>/clone="GLCCHR12"<br>/clone=lb="GLC"   | Query Match 58.5%; Score 188.8; DB 10; Length 661:<br>Best Local Similarity 99.0%; Pred. No. 1.4e-40.3; Indee O. Gane O.  |
| /thismue_type="corresponding non cancerous inver cissue" /der_stage="Admit" /lab_net="Sourcerous inver cissue" /nete="vector: paluescript sk(-); Site_1: EcoR1; Site_2:   | delines to Conservative Control of the Control of t          |
| ASE COUNT 205 a 141 c 112 9 162 t RIGIN   | Oy 127 aagacaggagccacatgcctacacagatgctgtggtgacgaggtccagagatacttg 186 Oy 127 aagacaggagccacatgcctacacagatgctgtggtgacgaggtccagagatacttg 186 Oy 127 aagacaggagccacatgcctacacagatgctgtggtgacgaggtccagagatacttg 186 Oy 112 aacaacacacacacacacacacacacacacacacacac  |
| Query Match 58.5%; Score 188.8; DB 10; Length 620; Best Local Similarity 99.0%; Pred. No. 1.3e-40; Matches 190; Conservative 0; Mismatches 2; Indels 0; Gaps 0;           |   |
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S. Dabil. Thornton M. Remachandran R. Whittington.J., Lerner, L. Krashoc. D. McElligott, K. Clark, S. Mays. R. Smith, E. Veloso. M. Hess. J. Cothren K. Lo.K. Offenbacher. J. Danzig. J. and Ducar. M.
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Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression
Nat. Biotechnol. 19 (5), 440 (2001) In press
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144 CAGCTAAATCCAGAAAATCAACGTGTAATGCAAAACGCGAGCCCTGCTGC 203
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BST16049 Athersys RAGE Library Homo sapiens CDNA, mRNA sequence.
BG196822
BG196822.1 GI:13718509
BG217233 802 bp mRNA EST 21-APR-2001
82756953 Athereys RACE Library Homo sapiens CDNA, mRNA sequence.
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Contact: Scott J. Cain
Athersys. Inc.
3101 Carnegle Ave. Cleveland, OH 44115, USA
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Location/Qualifiers
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TITLE OF INVENTION Colon and Colon Cancer Associated Polynucleotides and Polypept FILE REFERENCE: PAOLOGY.

FILE REFERENCE: PAOLOGY.

CURRENT FILEND DATE: 2002-03-27

PRIOR FILEND DATE: 2002-09-28

PRIOR FILEND DATE: 2000-09-28

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2440, Ap
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7. cgg12_6/ptodata/2/pna/JOS6_NEM_COMB.seq:*
GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                            OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Perfect score:
Sequence:
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124 tgcaagacagagccacatgccctacacagatgctqtggtgcacgaggtccagagatacc 183
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Best Local Similarity 53.14: Pred. No. 0.00014:
Matches 95: Conservative 0: Mismatches 84: Indels 0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PESULT 3
US-10-103-313-621
US-10-103-313-621
Sequence 621, Application US/10103313
Sequence 621, Application US/10103313
SEQUENCE 621
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PJ07C11
CURRENT FILM OANE: 2002-03-12
CURRENT FILM OANE: 2002-03-12
NUMBER 05 SD 10 MOS: 653
Frior Application removed - See File Wrapper or Palm
SOFTAME: Palentin Ver. 2.0
SD0 10 MC 621
LEMGTH: 1186
                                                                                                                                                                                                                                                                                                                                                                                              Query Match 17.6%; Score 56.8; DB 6; Length 526; Best Local Similarity 63.0%; Pred. Mo. 2e.08; Matches 85; Conservative 0; Mismatches 99; Indels 'Mismatches 85; Conservative 0; Mismatches 98; Conservative 0; Mismatche
                                                                                             NAWE/AET INSC. Geature
LOCATION: (519). (519)
OTHER INFORMATION: n equals a,t.g. or c
NAME/AET insc. desture
LOCATION: (223). (523)
OTHER INFORMATION: n equals a,t.g. or C
US-10-106-698-2440
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GENERAL INFORMATION:
APPLICANT: Rosen, et. al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : TYPE: DNA
: ORGANISH: Homo sapiens
US-10-103-313-621
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US-10-105-299-7204/c
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TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polyrer; ide
PILE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polyrer; ide
PILE REPERENCE: PAROSPI
CURRENT APPLICATION NUMBER: US/10/106,698
CURRENT APPLICATION NUMBER: US/010/26524
PRIOR APPLICATION NUMBER: US/01/26524
PRIOR APPLICATION NUMBER: US/01/26524
PRIOR APPLICATION NUMBER: US/01/26524
PRIOR PILICATION NUMBER: US/01/26524
PRIOR PILICATION NUMBER: US/01/26524
PRIOR PILICATION NUMBER: US/01/26524
SOFTHARE: PARCELLATION NUMBER: US/01/26524
67 gctcacatgccctacaccactgccgtgattcatgaggtgcagcgctttggggacatcgtc 126
                                                                                                 TXT: (332)..(332)
TXT: misc feature
(108: (336)
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LCCATION: (461). (462)'
OTHER INFORMATION: n equals a,t,g, or c
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OTHER INFORMATION: n equals a,t,g, or c
NAME/KET: misc_feature
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LOCATION: (4)...(4)
OTHER INPONANTION: n equals a,t,g.
NAME/KET: misc_feature
LOCATION: (23)...(23)...
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ORGANISM: Homo saplens
FEATURE:
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187 aagggaa 193
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260 a 260
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bb 9351 GCAGAACCGAACCTGTAGGAGCCCGCCCCCAACCTGATATCGCGTGTG 9292
cACAGAACCAACCAGACCTGTGGATAGGAGCAGCCCGCCCCCAACCTGATATCGCGTGTG 9292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9231 GGGCTGCGGGGACCCTCGACGCCACCTGCACACCTGCTGTCTGCCCCAAAGGT 9172
                                                                                                                                                                                                                                                                                      200 cagcctgccccatgcagtgacctgtgacattamattcagaaactatctcattcccaagg: 259
                                                                                                                                                                                                                                                   Db 1182 GCAGGAGCTGGACCCTGTGGTAGGTGGAGGCCGCCCCCAAGCCTGTCGCGTGG 1123
                                                                                                                                                                                                                            Ouery watch 12.0%; Score 3B 6; DB 6; Length 13327;
Best Locan Similarity 50:8%; Pred: No. 0.028; Indels 0; Gaps Matches 9; Conservative 0; Mismatches 89; Indels 0; Gaps
                                                                                                                                                                  Ouery Watch 1381, Score 44.6; DB 6; Length 1186; Best Local Similarity 53.14; Pred. No. 0.00014; Matches 9; Conservative 0; Hismatches 84; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 5

105-107-299-7201/C

Sequence 7201, Application US/10105299

SEREMAL IMPORATION:
CREERAL IMPORATION:
TITLE OF INVESTORS Haman Secreted Proteins
FILE REPERACE: PS95 Haman Secreted Proteins
FILE REPERACE: PS95 Haman Secreted Proteins
FILE REPERACE: PS95 Haman Secreted Proteins
FILE REPERACE: PS15 HAMAN SECRET APPLICATION NUMBER: US/10/105, 299

NUMBER OF SED ID NOS: 15197

FILE RAPELS PAREIT PAREIT NOS: 2.0

SED ID NO 7201

LEMPH: 13327
                             or Palm
  RESULT 8

19-0103-313-622

19-10103-313-622. Application US/10103313

19-0105-4-11700407104:

APPLICANT: Rosen et al.
2002-03-26
15197
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; ORGANISM: Homo sapiens
US-10-105-299-7201
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199 ccagcctgccccatgcagtgacctgtgacattaaattcagaaactatctcattccca 255
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9.31. Score 30.2; DB 6: Length 35959;
Best Local Similarity 52:84. Pred. No. 15;
Best Conservative 0: Mismatches 58; Indels 0;
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TION: COMPOSITIONS AND METHODS FOR THE THERAPY
TION: AND DIAGNOSIS OF CVARIAN CANCER
: 200121.495C1
                                                                                                                                                                                                                                                                                                                                                   RESULT 10
Sequence 10167, Application US/10105299
GENERAL INFORMATION:
TITLE OF INVENTION: Human Secreted Proteins
FILE REFERENCE: PS950
CURRENT APPLICATION Human Secreted Proteins
FILE REPRENCE: PS950
CURRENT PRILICATION HUMAN SECRETED PROTEINS
FILE APPLICATION HUMAN SECRETED PROTEINS
FILE APPLICATION HUMAN PROTEINS
FILE APPLICATION FOR PROTEIN FOR PROTEI
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TILLE OF INVENTION: COMPOSITIONS AND METHODS.
TILLE OF INVENTION: CAMPO DIAGNOSIS OF OVARIAN, FILLE OF INVENTION: AND DIAGNOSIS OF OVARIAN, FILLE OF INVENTION: AND DIAGNOSIS OF OVARIAN, CURRENT ELICATION NUMBER: US/10/015.219
SOFTHARE: FastSD (OF Windows Version 4.0 SD ID NO ID NO.
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: LOCATION: 440, 454, 480, 538, 559, 566, 587
: OTHER INFORMATION: n = A,T,C or G
US-10-015-219-101
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FILLE OF INTERFERENCE: RADOSPI
CURRETA FLILE. RADOSPI
CURRETA FLILE DATE: AND SPI
CURRETA FLILE DATE: 2002-10-27
CURRETA FLILE DATE: 2002-10-27
PRIOR PELINE DATE: 2002-10-27
PRIOR APPLICATION NUMBER: US/10/163/2624
PRIOR PELINE DATE: 2009-90-28
PRIOR PELINE DATE: 1999-09-29
PRIOR FILLING DATE: 1999-11-01
PRIOR FILLING DATE: 1999-11-01
SPIOR FILLING DATE: 1999-11-01
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CURRENT APPLICATION WINGER: US/09/75,254
PRIOR APPLICATION WINGER: US/09/75,3191
PRIOR FILING ANTE: 1999-03-05
SED ID NOS: 31255
SED ID NOS: 31255
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9.7%, Score 31.4; DB 6; Length 998;

Best Local Similarity 57.3%, Pred. No. 1.4;

Matches 50; Conservative 3; Wismatches 34; Indels 0: Gaps
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: OTRER INFORMATION: Clone ID: 700955037H1

US-09-975-254-18019
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US-10-106-698-892
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Sequence 18019, Application US/09975254
GENERAL INFORMATION:
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ORGANISM: Bomo sapiens
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RESULT 12
US-10-105-299-2978
' Sequence 2978, Application US/10105299
"Several INFORMATION:
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APLICANT: MIZUNO, SHUICHI
APPLICANT: GLOWGELS, JULICHI
APPLICANT: GLOWGELS, JULICHI
TILLE OF INVENTION: DIAGNESIS AND TREATHENT OF SKELETAL DEGENERATION CONDITIONS
TILLE REPERRORE: B0001/7244/KA/PEF
CURRENT APPLICATION WINDER: PCT/V302/07787
CURRENT APPLICATION WINDER: 35 60/274,980
PRIOR RELING DATE: 3001-03-12
NUMBER OF SEQ 1D NOS: 79
SOFTWARE: PARCELLING TOWNS: 79
SOFTWARE: PARCELLING TOWNS: 79
     4117 atgggttgctagaggatggtagaactggaagcaaggcagctacctttttgcaaaaggaaa 4176
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9.11: Frore 20.4; DB 1; Length 7694:
Best Local Similarity 56.31: Fred. No. 14;
Matches 34; Conservative 0; Manches 41; Indels 0
                                                                                                                                                                                                                            e Brigham and Womer s Hospital. Inc.
ates, Karen
izuno, Shuichi
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TIILE OF INVENTION: Human Secreted Proteins
FILE REFERENCE: PS950
                                                                                                                                                                               IT-USO2-07787-34/c
Sequence 34, Application PC/IUS0207787
GENERAL INFORMATION:
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US-10-105-299-9480/c
: Sequence 9480, Application US/10135299
: GENERAL INFORMATION:
                                                                                            4177 tggtgttaggcccttttccaga 4199
                                               155 tgctgtggtgcacqaggtccaga 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : TYPE: DNA
: ORGANISH: Homo sapiens
PCT-US02-07787-34
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: ORGANISM: Homo sapiens
US-10-105-299-9480
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134 CTCCATAATTGTTACATTATCATTGCCAGGGTTCTCCTCCTGCTCTAGCTTTTGCTGGT 175
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736 tocciticcagittigicigiaagaggaagtgatcagagaaatcaaaaaagagaag 795
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NUMBER OF EQ. 2002-03-26
NUMBER OF EQ. 2D MOS: 15197
Prior Application removed See File Wrapper or Palm SOFTWARE: Patentin Ver. 2.0
LENTH: 1103
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                                                                 APPLICANT: Rosen, et. al
TILE OF INVENTION: Human Secreted Proteins
                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Human Secreted Protein
FILE REPERENC: PS950
CURRENT APPLICATION NUMBER: US/10/105,299
CURRENT FILING DATE: 2002-03-26
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US-10-105-299-14978
: Sequence 14978, Application US/10105299
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TTPE: DNA : ORGANISM: Homo sapiens US-10-105-299-14978

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Ouery Match
Best Local Similarity 50.31
Matches 72; Conservative

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; TIPE: DNA ; ORGANISM: Homo sapiens US-10-105-299-2978

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Page 1

|  | GenCore version 4.5  | Result<br>No.        | Score  | Query<br>Match Length                             |   | 11 BG              |
|--|--|----------------------|--------|---|---|--------------------|
|  | Copyrignt (c) 1993 - 2000 Compugen Ltd.  |                      |        | 9.66  | 1746                                      |                    |
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| Run or.:                               | April 19, 2002, 07:21:40; Search time 4168.4 Seconds (Without alignments)  | 4 N O I              | 1534.6 | 87.9<br>87.9                                      | 1852                                      | 1 4 4 1<br>0 0 0 0 |
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| Searc!.ed:                             | 1472140 seqs, 8248589755 residues  | 16                   |        |   | 1576                                      |                    |
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|  |  | 37                   |        |   | 1737                                      |                    |
|  | 11: gb_sts:*<br>2: gb_sy:*   | 36                   |        |   | 2340                                      | • •                |
| -                                      | (3: gb_un:*<br>(4: gb vi:*   | <b>*</b>             |        |   | 1662                                      | <b>~</b> ~         |
|  |  | 42                   |        |   | 1871                                      | α.<br>•            |
|  | 16: en_fun:*<br>17: en_hum:*   | E # #                | 1050   | 59.1<br>59.5                                      | 1579                                      |                    |
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| • • •                                  |  | DEFINITION           | z      | dience 2  | from p                                    | atent              |
| .,                                     | 28: em_un:*<br>29: em_vi:*   | ACCESSION<br>VERSION |        | AR071575<br>AR071575.1 GI:7222463                 | G1:72                                     | 22463              |
| • •                                    |  | KEYWORDS             | s      |   |   |                    |
| 1                                      | 31: em_htgo_inv:*<br>32: em_htgo_rod:*   | SOURCE<br>ORGANISM   | MSIN   | Unknown.<br>Unknown.                              |   |                    |
|  |  | 4                    |        | Unclassified.                                     | ed.                                       | 19                 |
|  | 34: em_ntg_inv:*<br>35: em_htg_rod:*   | AUTHORS              |        | Goldstein, J.A. and De                            | J.A. an                                   | d De               |
| . 1                                    |  | TITLE                |        | Cloning, expression and<br>the principal determin | xpressi<br>pal det                        | on an<br>ermin     |
| Pred. No.                              | Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed. | JOURNAL<br>FEATURES  | ۳ د    | Patent: US 5912120-A 2<br>Location/Qual<br>1 1746 | JS 5912120-A 2<br>Location/Qual<br>1 1746 | 0-A 2<br>/Oua)     |
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SUMMARIES

ALIGNMENTS

Page 2

| Oy 1021 tgcacgacaggggcacatgccctacacagatgctgtggtgcacgaggtccagagataca 1080 1021 TGCAGGACAGGGCCACATGCCCTACACAGATGCTGTGCACGAGGTCCAGAGATACA 1080 1021 TGCAGGACAGGGCCCACATGCCCTACACAGATGCTGTGGTGCACGAGGTCCAGAGATACA 1080 Oy 1081 tgcactcaccaccagcctgccctacagcctgacctgagatgtaattcagaacat 1140 1161 1161 1161 1161 1161 1161 1161 116 | 0y         1141 acctcattcccaaggcacaaccatattaacttcctcacttctgtgctacatgacaaca         1200           b         1141 ACCTCATTCCCAAGGCACAACCATATAACTTCCCTCACTTCTGTGCTACATGACAACA         1200           0y         1201 aagaatttcccaaccaagaatttttaacctgtcacttctqatqaagatgaaatt         1260           0y         1101   | 0y         1261 ttaagaaagtaactacttcatcatcatgcctttctcagcagaaaggattggtgggaagg 1320           1261 Itlaffffffffffffffffffffffffffffffffffff | Oy 1381 actor(equatocoa) agacctique coa) coccidintification (140 constitution) (150 const | Oy 1501 etectgractgractgragetetetteetetggreeaaatteactgraggget 1560  | ICTICTGACCCGTCATCTCACATTTTCCCTTCCCCCAAGATCTAGTGAACATTCAGCCTC CattaaaaagttCcactggcaaatatatctgctattccccatactataagttac HHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH | Oy 1681 attgatgccacatatgctgatacttgcctatgtggttattacattattatta 1740 LILIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII | HESULI 2                       | DRUMNISH THE THE TREATOR: Chordate: Craniate: Vertebrate; Euteleostomi; Eukaryote: Metazoa: Chordate: Catarrhini; Hominidae: Homo.  REFERENCE 1 (bases 1 to 1146) AUTHORS Romess.M., Faletto.M.B., Blaisdell.J.A., Raucy.J.L. and Coldstein.J.A. and Coldstein.J.A. and Coldstein.J.A. and Coldstein.J.A. and Coldstein.J.A. and Expression of Complementary DAMs for multiple members of the human cytochrome P45011c subfamily [published erratum appears in Blochemistry 1993 Feb 9.3215):1390]  JOURNAL Blochemistry 30 (13), 3247-3255 (1991) |
|---|--|--|--|---|---|---|--------------------------------|--|
| tch 201 Similarity 99.6%; Score 1739.6; DB 6; Length 1746; 2021 Similarity 99.8%; Pred. No. 0; 1742; Conservative 0; Hismatches 4; Indels 0; Ga ctroatgatccttgtggtcctggtcctgtctctctcatgatttgcttcttcaa   | CTCANTIGATECTITION GOLD TO THE CENTRE OF THE CENTR OF THE CENTRE OF THE CENTR OF TH | 181 aaatetagecetgytteeteetgattttgecetgaaegeagegegegegegeg 180 181 hillillillillillillillillillillillillill                               | atticcectggcgaaagagctaccagagatitggaatcgtitcagcaatggaaag<br>  | uniconomismic concentration control of the control |   | 601 aaaaattgaatgaaaacatcaggattgtaagcacccctggatccagatatgcaataatt 650                                     | acaccaagaatcgatggacatcaaca<br> | ### ### ##############################   |

| PEATURES     | URES                                 | Location/Qualifiers  | ò              | gatatgaagtggtgaaggaagccctgattgatcttggagaggggtttctggaagagggcc<br>  |
|--------------|--------------------------------------|--|----------------|---|
|              |                                      | /organism="Homo sapiens"   | <b>q</b> O     | 241 GATATGAAGTGGTGAAGGAAGCCCTGATTGATCTTGGAGAGGAGTTTTCTGGAAGAGGCC 300  |
|              | mRNA                                 | 6. 1478  | ο,             | 301 atticccactggctgaaagagctaacagaggatitggaatcgtttcagcaatggaaaga 360   |
|              | dene                                 | /year caracts  | qa             | 301 ATTICCCACIGGCIGAAAGAGCIAACAGAGATITGGAATCGIITTCAGCAAIGGAAAGA 360   |
|              | cDS                                  |  | λc             | 361 gatggaaggagattcggcgtttctccctcatga <u>cgctgcggaattttggggaagg</u> 420   |
|              |                                      | /gene=_Crrzis<br>/codon_start=1  | a              | 361 GATGGAAGGAGATCCGGCGTTTCTCCCTCATGACGCTGCGGAATTTTGGGATGGGGAAGA 420  |
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|              |                                      | /translation="MDPFVVLVLCLSCLLLLSIWRQSSGRGKLPPGFTPLFV1GN1LQ<br>IDIKDVSKSLINLSKITGPVFTLYFGLERNVVLRGTEVVREALIDLGEEFSGRGHFFL   | <b>Q</b> G     | GGAGCATTGAGGACCGTGTTCAAGGAAGCCCGCTGCCTTGTGGAGGAGTTGAGAAAAA  |
|              |                                      | ABRANRGPG IVFSNGKRWREI RRESLATLRNFGMGKRS I EDRVOERARCLYEELK I TK<br>ABPODPT FILOCADEWY I CSI I FOR RROYK DAQDE LAHEK LABNIN 18TIF YET GY OLGN<br>PPPT I TOP FOCH WILL KNIA PRESDIL KRVKEHDESMOI NYROFF I DCFLI KWEKEKO   | VC<br>do       | 481 ccaaggcttcaccctgtgatcccactttcatcctgggctgtgtcccgggattgtatct 540  |
|              |                                      | NQQSEFTIENLVITAADLLGAGTETTSTTLRYALLLLEKHPEVTAKVQEETERVIGEN<br>RSPCMODRGHMPYTDAVVHEVQRYIDLIPTSLPHAVTCDVKFENYLIPRGTIILTSLI   | ζŞ             |   |
|              | :                                    | adnkefpnp<br>dnfnlksli   | <b>q</b> o     | 541 GCICCATIAITIICCAGAAACGIITCGATTAIAAAGATCAGCAATTICTIAACTTGATGG 600  |
|              | old_sequence                         | 782<br>782   | οy             | 601 aaaaattgaatgaaaacatcaggattgtaagcacccctggatccagatatgcaataatt 660   |
|              | •                                    | /citation=[i]<br>/replace="a"<br>/re   | qo             | 601 AAAATIGAATGAAAACATCAGGATTGTAAGCACCCCCTGGATCCAGATATGCAATAATT 660   |
|              | annae Toro                           | ) // // // // // // // // // // // // //   | λ6             | 661 tteccactateattgattattteeegggaacecataacaaattaettaaaaacettgett 720  |
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|              |                                      | /gene-"Crp2c19"  | oy.            | ttatggaaagtgatattttggaaaagtaaaagaacaccaagaatcgatggacatcaaca   |
|              | old segmence                         | /replace='gc'<br>1250. 1251  | qd             | TTATGGAAAGTGATATTTTGGAGAAAGTAAAAGAACACCAAGAATGGATGG   |
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|              | 710                                  | /replace"ac"   | q <sub>Q</sub> |   |
|              | acmanhag nro                         | .vo.t.<br>/vote="addition of t"<br>/citation=[1]   | λο t           | 841 agtctgaattcactattgaaaacttggtaatcactgcagctgacttactt  |
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| 88           | Query Match<br>Best Local Similarity | 99.64; Score 1739.6; DB 9; Length 1746;<br>99.84; Pred. No. 0;   | S da           | 1021   tycacqacagggyccacatgccctacacagatgctgtygtycacgaggtccaggataca   1080   |
| ž į          | Matches 1742; Conservative           | servative 0; Mismatches 4; Indels 0; Gaps 0:   | ٥٨             | 1081   togacetcatececaceagetyceceatycaytyaectytyaegteaatteayaaaet   1140  |
| \$ E         | 1111111                              |  | qc             |   |
| 8 6          | 61 tctggagac                         | 61 tctggagcagagcagctctgggaggaaaactccctctggcccactcctcccagtga 12)  | 23             | 1141 acticaticoccaaggcacaaccatatiaacticoctocaticigggtacaggcacaacticaticoctaaticiggggacagcaacaatiaacticoctocaticiggggacaggcacaacticatiatiiiiiiiiiii  |
| 윱            | 61 TCTGGAGAC                         | GAGCICIGGGAGAGAAACICCCICCIGGCCCCACICCICICCCAGIGA 129   | o,             |   |
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| 6 8          | 181 AAATCTATG                        |  | q å            | 1261 ITAAGAAAGTAACTACTICAJGCCTITCTCAGCAGAAAAGGGATTIGTGTGGGAGGGG 1320 1321 gcctdgcccgcatdgagctqttttattcctqaccttcattttacagaactttaacctga 1380  |

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| Letent: JP 1998033166-A 2 10-FEB-1998;
| LIOMOGI & CO LTO
| Homos apiales (human)
| JP 1998033166-A2
| 10-FEB-1998 | 199613015
| BABA TAKAHIKO, KIRITA SHIRO, AOTAMA JUNKO
| BABA TAKAHIKO, KIRITA SHIRO, AOTAMA JUNKO
| CI2NS/02,CO7H21/04,CO7K1/16,CIZNI/21,CIZNIS/09,(CI2NS/02,
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Location/Qualifiers
1. 1669

    1669
    /organism-'Homo sapiens'
    /tissue_type-'liver'
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JP 1998033166-A/2.
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Cloning, expression and diagnosis of human cytochrome P450 2C19: the principal determinant of s mephenytoin metabolism Paten: 108 5917120-4 15-JUN-1999; Location/Qualifiers 1. 1854
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Ronkes.M., Faletto.M.B., Blaisdell.J.A., Raucy,J.L. and
Goldstein.J.A.

Cloning and expression of complementary DNAs for multiple members
of the human cytochrome P45011C subfamily [published erratum
appears in Blochemistry 1993 Feb 9:32(5):1390]
Blochemistry 30 (13), 3247-3255 (1991)
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HUMCTP2C9 1854 bp mRNA PRI 31-DEC-1994 buman cytochrome P4502C9 (GTP2C9) mRNA, clone 25. W61852 00336 de fill 18101 clone 25. Cytochrome P450 cytochrome P450

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|   | 73 tggaaagtgtattttggagaagtaaagtaaagtaacccagaactgatgaacccg  | 1137 TCATCCCAAGGGCAAACAATTAATTCCCTGCTTCTGTGCTAACAGCAAGG 1195 1204 aatttcccaacccagagatgtttgacctcgtcacttctggatgaagtggaaattta 1253 1197 AATTCCCAAGCCAAGATTTGTGTTTTTTGTGTGTGAAAAGGTGCAATTTA 1256 1254 agaaaataactacttcatgcctttctcagaagaaaacggatttgatggggaagggcc 1323 1111111111111111111111111111111111  |

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Mammalia; Eutheria: Primates: Catarrhini: Hominidae; Homo.
Olgises: Loo 1814)
Olgiya. S., Amoni. M., Shiramatsu. K., Shinriki. N. and
Kamatski. T.
Six base deletion occurring in messages of human cytochrome P-450
in the CYP2C subfamily results in reduction of tolbutamide
                                                                                                                                                                   1396 caaagacctgacacaactcctgttgtcaatgaattgcttctgtcccgccttctatc 1455
1382 cAAAGAACTTACACCCCAATTGTAATTAGTTGCGCCTCTTCACC 1441
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1502 TGCAGCTETTTTCTTGTGTTATGCATCTTGGACTATGTATGCTTTTCT 1561
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1622 GAGAGTITCCTATTTACTGTGCAAATATATGCTGTATTCTCCATACTGTAACKI 1681
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Putative CYPC2C9 gene (human, liver, mRNA, 1814 nt)
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| Oy 583 aatticitaacttgatggaaaatt Db 541 AATTCTTAACTAATGCAAAAGT Oy 643 tccagatatgcaataatttccac Oy 601 tccagatatgcaataatttTTTTTC Oy 703 tacttaaaaccttgctttatgga Db 661 TACTTAAAAACGTGCTTTAATGG |  | 961<br>1063<br>1021<br>1123<br>1081  | Oy 110) Cigracange against the control of the contr | 0y 1363 tacagaacttiaacctgaaaictcu  | 0y 1483 gerogatgatctgctgctcctgt, Db 1441 GAGCAGATGGCCTGCTGCTGTTTTTTTTTTTTTTTTTTT                      |
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| hydroxy<br>Blochem<br>9307524<br>GenBank<br>entry i<br>This<br>This<br>Contain  | geee 1. 1814  CDS 3. 143 c 146  CDS 7. 145  CDS 7. 145  CDS 7. 146  CDS 7. 146  CDC 7. 1814  CDC 7. 1815  CDC | #5.7%; Score 1495.8; rity 92.8%; Pred. No. 0; aservative 0; Mismatches tecttreacteggagacagagactetg | dy       103 cortectercecaegeatgaatacetacagatagatataaggatgtcagcaal 162         bb       101  | Oy         283 agttttctggaagagcatttcccactggctgaaagagctaacagaggatttggaatcg         342           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII | 0y 403 atttgggatgggaagaggattgaggaccgtgttcaagaggaagccgtgccttg 462  11111111111111111111111111111111111 |

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Homo sapiens (human)
Mataryota, Metazona Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
Butheria; Primates; Catarrhini; Hominidae; Homo.
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# 15-JUL-1994 JP 94P 19P 1906-1993 JP 93P 201150
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# RAVEN ROMENT KOLFIRSO, NAKATSURA 18AO
# C1201/02-C12N/34,C1201/26;
# KANENO HIDDO, NAKATSURA 18AO
# C1201/02-C12N/34,C1201/26;
# KANENO HIDDO, NAKATSURA 18AO
# C1201/02-C13N/34,C1201/26;
# C1201/02-C13N/34,C1201/26;
# C1201/02-C13N/34,C1201/26;
# C1201/02-C13N/34,C1201/26;
# C1201/02-C13N/34,C1201/26;
# C1201/03-C13N/34,C1201/26;
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//organism="Homo sapiens"
1. .1473
/product="human cytochrome P450 2C19"
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/db_xref-"taxon:9606"
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Sendate, M., Faletto, M. B., Blaisdell, J. A., Raucy, J. L. and Goldatein, J. A., Faletto, M. B., Blaisdell, J. A., Raucy, J. L. and Correction: Cloning and expression of complementary coNAs for multiple members of the human cytochrome P450IIC subfamily Homomery of the Mamma Cytochrome P450IIC subfamily Biochemistry 32, 1390-1390 (1993)
Biochemistry 32, 1390-1390 (1993)
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Resequencing demonstrated that it is not a separate gene, but is a splice variant or a composite coNA. The 5' portion corresponds to a partial 2018 clone, and the 3' portion corresponds to a partial 2018 clone.
The 5' end from 1 to 911 corresponds to a partial allelic variant or 2 colle beginning a base 501 of 2018 contiuning through base pair 1019 colling for 11e 129 instead of Met 129 and 5 to A change at 307 coding for 11e 129 instead of Met 129 and 6 to A change at bp 1004 coding for 10a13 instead of Met 129 and 6 to A change at bp 1004 coding for 10a13 instead of Met 129 and 6 for 0 through base split 1612. Seconds of 2018 (beginning of exon 2) through base split 1612. Seconds of 2018 (beginning of exon 2) through base split 1612. Seconds from the previously reported 2019 sequence.
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JP 1998033166-A/1
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Artificial gene for hum
protein.
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PP C121-19)
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VERSION
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SOURCE
ORGANISM
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AUTHORS
TITLE
                                                                                                                                                                                                                                                                           1381
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a õ CHORENT

us-09-763-292-1.rge

| RESULT 15  |  | qq     | 24]  |
|------------|--|--------|------|
| LOCUS      | HUMCIPMPA 1577 bp mRNA PRI 02-NOV-1994                                 | ċ      | 330  |
| DEPINITION | S-mephenytoin 4-hydroxylase  | ;      | ,    |
|            | 3' end, clone MP-8.  | £      | 301  |
| ACCESSION  | M21939 J02832  | 1      |      |
| VERSION    | M21939.1 GI:181363   | c      | 380  |
| KEYWORDS   | cytochrome; cytochrome P450; cytochrome P450 S-mephenytoin             | 5      | 5    |
|            | 4-hydroxylase.   | ď      | 361  |
| SOURCE     | Human liver, cDNA to mRNA, clone MP-8.                                 |        |      |
| ORGANISM   | Bomo sapiens   | ċ      | 440  |
|            | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata: Euteleostomi:      | •      |      |
|            | Mammalia, Eutheria, Primates, Catarrhip! Hominidae: Homo.              | £      | 42   |
| REFERENCE  | 1 (bases 1 to 1577)  | 2      | •    |
| AUTHORS    | Ged, C., Umbenhauer, D.R., Bellew, T.M., Bork, R.W., Srivastava, P.K., | ::0    | 200  |
|            | Shinriki, N., Lloyd, R.S. and Guengerich, F.P.                         | î      |      |
| TITLE      | Characterization of cDNAs, mRNAs, and proteins related to human        | QQ     | 48]  |
|            | liver microsomal cytochrome P-450 (S)-mephenytoin 4'-hydroxylase       | 1      |      |
| JOHNAT     | Biochemistry 27 (18), 6929-6940 (1988)                                 | ć      | 2,66 |
| MEDLINE    | 89062423   | ÿ      | ,    |
| COPORENT   | Cytochrome P-450 is a multigene family coding for several related      | t<br>d | 54.3 |
|            | human liver enzymes. The term P-450mp is used in a generic sense       |        |      |
|            | to include all of the proteins related to P-450mp-1, P-450mp-2, and    | č      | 620  |
|            | P-450Bp-3.   | ï      |      |
| FEATURES   | Location/Qualifiers  | gg     | 601  |
| source     | 1. 1577  |        |      |
|            |  |        |      |

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SPTPLPVIGNILQIGIKD
LGEEFSGRGIFPLAERAN
EARCLVEELRKTKASPCD
KILSSPWIQICNNFSPII
                                                                   VQEEIERVIGRNRSPCM
IPKGTTILISLTSVLHD
ALAGMELFLFLTSIION
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droxylase,
                                                                                                                                      3; Gaps
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Search completed: April 19, 2002, 09:24:59 Job time: 7399 sec

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| 4.5             | Compugen Ltd.             |
| GenCore version | Copyright (c) 1993 - 2000 |

| Run on:                               | April 19, 2002, 07:21:40 ; Search time 277.57 Seconds<br>(without alignment) years (\$592.897 Hillion cell updates/sec |
|---------------------------------------|--|
| Title:<br>Perfect score:<br>Sequence: | US-09-763-292-1<br>1746<br>1 cttcaatggatccttttgtgacatattattattaaataga 1746   |
| Scoring table:                        | IDENTITY_NUC<br>Gapop 10.0 , Gapext 1.0  |
| Searched:                             | 930621 seqs, 428662619 residues  |
| Total number of                       | Total number of hits satisfying chosen parameters: 1851242   |
| Minimum DB seq<br>Maximum DB seq      | Minimum DB seq length: 0<br>Maximum DB seq length: 2000000000  |
| Post processing                       | Post-processing: Minimum Match 01 Maximum Match 1001 Listing first 45 summaries  |
| Database :                            | N_Geneseq_1101:*<br>1: /SIDS2/gcgdata/geneseq/geneseqn/NA1980.DAT:*  |

1170 1109.8 1109.8 1109.8 1106.6 1106.6 1106.6 1105.6 645.2 627.2

Human liver cytoch Human cytochrome P4(3) 2 Cytochrome P4(3) 3 Cytochr

## 2: /51082//gcidate/jeneseq/jeneseqn/kNi981.phT: 4: /51082/gcidate/jeneseq/jeneseqn/kNi981.phT: 4: /51082/gcidate/jeneseq/jeneseqn/kNi981.phT: 5: /51082/gcidate/jeneseq-jeneseqn/kNi981.phT: 6: /51082/gcidate/jeneseq-jeneseqn/kNi981.phT: 7: /51082/gcidate/jeneseq-jeneseqn/kNi981.phT: 8: /51082/gcidate/jeneseq-jeneseqn/kNi981.phT: 9: /51082/gcidate/jeneseq-jeneseqn/kNi981.phT: 10: /51082/gcidate/jeneseq-jeneseqn/kNi981.phT: 11: /51082/gcidate/jeneseq-jeneseqn/kNi991.phT: 11: /51082/gcidate/jeneseq-jeneseqn/kNi991.phT: 11: /51082/gcidate/jeneseq-jeneseqn/kNi991.phT: 11: /51082/gcidate/jeneseq-jeneseqn/kNi992.phT: 11: /51082/gcidate/jeneseq-jeneseqn/kNi992.phT: 11: /51082/gcidate/jeneseq-jeneseqn/kNi992.phT: 11: /51082/gcidate/jeneseq-jeneseqn/kNi995.phT: 12: /51082/gcidate/jeneseq-jeneseqn/kNi999.phT: 13: /51082/gcidate/jeneseq-jeneseqn/kNi999.phT: 14: /51082/gcidate/jeneseq-jeneseqn/kNi999.phT: 15: /51082/gcidate/jeneseq-jeneseqn/kNi999.phT: 16: /51082/gcidate/jeneseq-jeneseqn/kNi999.phT: 17: /51082/gcidate/jeneseq-jeneseqn/kNi999.phT: 18: /51082/gcidate/jeneseq-jeneseqn/kNi999.phT:

Pred. Mo. is the number of results predicted by chance to have a scree greater than or equal to the score of this result being printed, and is derived by analysis of the total score distribution.

## | Percent | Context | Cont

| RESI   | RESULT 1                      |  |
|--------|-------------------------------|--|
| =      | AAV44153 standard: CDNA: 1746 | . CDNA: 1746 BP  |
| ×      |                               |  |
| A<br>A | AAV44153;                     |  |
| ×      |                               |  |
| IC     | 06-OCT-1998 (first entry)     | st entry)  |
| ×      |                               |  |
| 30     | Human cytochrome              | Human cytochrome P450 2C19 clone 11a cDNA.                           |
| ×      |                               |  |
| ¥.     | Cytochrome P450;              | Cytochrome P450; drug screening; S-mephenytoin 4'-hydroxylase;       |
| X<br>N | identification: m             | identification: mutagenic: carcinogenic: cytotoxic: haemoprotein;    |
| X      | xenobiotic; envir             | xenobiotic; environmental pollutant; ss.                             |
| ×      |                               |  |
| SO     | Homo sapiens.                 |  |
| ×      |                               |  |
| Z,     | US5786191-A.                  |  |
| X      |                               |  |
| PD     | 28-JUL-1998.                  |  |
| ×      |                               |  |
| Ġ.     | 22-FEB-1994; 94               | 94US-0201118.  |
| XX     |                               |  |
| PR     | 22-FEB-1994; 94               | 94US-0201118.  |
| P.R    | 09-APR-1992; 92               | 92US-0864962.  |
| ×      |                               |  |
| P.A    | (GOLD/) GOLDSTEIN J A.        | J.A.   |
| ΡA     | (ROMK/) ROMKES-SPARKS M.      | ARKS M.  |
| ×      |                               |  |
| ΡI     | Goldstein JA, Ro              | Romkes-sparks M;   |
| X      |                               |  |
| DR     | WPI; 1998-436528/37.          | 37.  |
| ×      |                               |  |
| 14     | Screening for dru             | Screening for drugs metabolised by cytochrome P450 - for identifying |
| 4      | mutadenic carcin              | mutadenic carcinogenic or extotoxic compounds                        |

Page 2

###888888888

| This   | 102 transparsagggcearatggcearagggattcaggggaaaccgggaalaca<br>103 tggacgacggggcacatggcccaagaggacggggggaaacagaaca<br>104 transparsaggggcacatggcccaagaggacgtggagggaaact<br>108 tggactcatcccaagggcacacatgacgggaactggagggaaactggggaaact<br>119 transparsagggcacacacatggacgggaacttgacgggaaactggggaaact<br>110 tgactcatcccaagggcacacacattaacttcccattcggggaaactggaaact<br>111 acctcattcccaagggcacacacattaacttccctacttcggggaaact<br>1120 aagaatttcccaagggcacacacattaacttccctaacttcggggaaact<br>111 | ANJ12241 standard: CDNA; 1748 BP.<br>XX AAD12241;<br>XX XX               |
|--|--|--|
| Example 2; Column 35-38; 63pp: English.  This sequence encodes a cytochrome P450 2C19 polypeptide isolated for a first manner clone in a This polypeptide is used in a method to Screen for a drug that is metabolised by a cytochrome P450 having 5-mephenyton by 4 "hydroxylase activity. The protein can also be used to identify as mitagonic, carcinogenic or cytochrotic compound. Cytochrome P450 are a large family of hamoprotein enzymes capable of metabolising xenobiotics such as steroids, fatty acids and environmental pollutants as well as endobiotics such as steroids, fatty acids and prostaglandins.  Sequence 1746 BP; 477 A; 418 C; 365 G; 486 T; O other; | Score 1739,6: DB 19: Length 1746:  Pred. W. O.  Pred. W. O.  Pred. W. O.  11   | agtaabagaacaccannininininining<br>cctgatcaaaatggagaaggaaaggaaaaccaac 840 |

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cattcccaagggcacaaccatattacttcctcctcttgtgctacatgacaca 1200
                                                                                                       tgaccogtcatctcacattttcccttccccaagatctagtgaacattcagcctc 1620
                                                                                                                                                  .....tgacccgtcatctccacattttcccttcccccagatctagtgaacattcagcctc 1620
                                                                                                                                                             la 1746
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Ruman; gene structure; phenotypic expression; guanosine cofactor;
germilare variation analysis; exon-intron boundary; Tetrahymena rRNA;
eyrochrome P40 2C19; C7F450 2C19; ss.
                                                                                                                Location/Qualifiers

9.10

7.tag-
40.59

7.bound_molety-
7.tag-
Dound_molety-
7.tag-
Complement (43..57)

7.tag-
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7.00..37

7.00.01.00.01.00..527)

7.4147 1.00..537

7.00.01.00.01.00..537)

617..638 7.00..639

617..638 7.00..639

7.41437 7.00.01.00..699)
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/*tag- n
/*Cound_moiety- *Primer 6800*
Complement (784..802)
/*tag- n
/*Cound_moiety- *Primer 784U*
                                                                                                                                                                                                                                                                                                                                                                                                                                      Chound_moiety= "Primer .349L"
complement (367..386)
/*tag= j
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ind_molety= "Primer 367U"
..527
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cound_molety- 'Primer 790L'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tag" q
Ound_molety" "Primer 947L"
mplement (948..962)
                       Human cytochrome P450 (CYP450) 2C19 cDNA
25-SEP-2001 (first entry)
                                                                                                                Key
misc_signal
                                                                                           Homo saplens.
                                                                                                                                                                 primer_bind
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Abound moiety. Primer 1106L'
Abound moiety. Primer 1106L'
Abound moiety. Primer 1108U'
Complement (1215..1229)
Aug State of the complement (1215..1229)
Complement (1215..1229) /\*tag- ae Chound\_moiety- \*Primer 1522L\* complement (1700..1717) /\*tag- af // Chound\_moiety- \*Primer 1670U\* /bound\_molety= "Primer 1063L" complement (1064..1079) nd\_moiety= "Primer 10640" ..1121 Dound\_molety= "Primer 1231U" 1238..1259 ^\*tag= aa /bound\_molety- \*Primer 1238L\* complement (1420..1439) /\*tag- ab /bound\_molety- \*Primer 1396U\* 1422..1443 /\*tag= ac /bound\_moiety= "Primer 1392L" complement (1549..1568) /\*tag- ad //bound\_moiety- "Primer 1519U" 1552..1573 /\*tag- ag /bound\_molety- "Primer 1690L" (GENO-) GENOME THERAPEUTICS CORP. 17-JAN-2001; 2001WO-US01451. 20-JAN-2000; 2000US-0488127 Thomann H, Fitzgerald MS: WO200153529-A2. primer\_bind 26-JUL-2001. primer\_bind primer\_bind

WPI: 2001-465380/50.

Determining structure of genes whose sequence is not known from cDNA, by sequencing the gene or gene across exon intron boundaries using evenly spaced primers comprising nucleic acids that hybridize to the CDNA of gene

Example 2; Fig 3; 81pp: English.

The present invention relates to a method for determining gene sequencing when the genomic sequence is unknown. The method involves sequencing the gene across son-intron boundaries using evenly spaced pithers or tiled primers. The tiled primers comprises moteled acids that hybridise to the known this sequence of the gene at about 100-300 hase fletermined without the need to sequence the entire gene. The method expression without the need to sequence the entire gene. The method expression without the need to sequence entire chromosomal copy of the analysis. The method is also useful in germine sequence variation analysis. The method is also useful of the gene or fragment. The method are useful of the performance of the gene of fragment. The method is also useful or general the boundaries expense regions of mutleic acids that Veries separated by intervening sequence and also for determining boundaries present in genes containing group i type introns such as Tetrahymena TRNA, where self-splicing occurs

| 961 tcacagctaaagtccaggaagaattgaacgtgtcattggcagaaaccggagccctgca<br>  | 1083  |   | 1261   traspassatasctacttcatgcctttctcaggaaaacggattgtgtggggagagg   1111 | 13.3 godrygodogogogogottitlaticotoacottoatitlatogoacottoaotti<br>1381 aatottottoattoacotaaogoacottoaoacoactottyttoatogottyottotto<br>1111111111111111111111111111  | 1441 1443 1501   |   | 162) cattaaaaaagtttcactgtgcaaatatatctgctattccccatactc' | logi attgatgicacaaaagggatattigitaaagggatattaaaaaaaaaa              | EESULT 3<br>AAT03708<br>10 AAT03708 standard; CDNA; 1745 BP.                | AT03708:  10 06-SEP-1996 (first entry)  21 Cytochrome P450 2C19 cDNA.  22 Cytochrome P450 2C19; human: liver; PCR; primer; detection;  23 Cytochrome P450 2C19; human: liver; PCR; primer; detection;  24 Cytochrome P450 2C19; human: liver; PCR; primer; detection;  25 Cytochrome P450 2C19; human: liver; PCR; primer; detection;  26 Cytochrome P450 2C19; human: liver; PCR; primer; detection;  27 Cytochrome P450 2C19; human: liver; PCR; primer; detection;  28 Cytochrome P450 2C19; human: liver; PCR; primer; detection;  28 Cytochrome P450 2C19; human: liver; PCR; primer; detection;  29 Cytochrome P450 2C19; human: liver; PCR; primer; detection;  20 Cytochrome P450 2C19; human: liver; PCR; primer; detection;  20 Cytochrome P450 2C19; human: liver; PCR; primer; detection;  20 Cytochrome P450 2C19; human: liver; PCR; primer; detection;  20 Cytochrome P450 2C19; human: liver; PCR; primer; detection;  21 Cytochrome P450 2C19; human: liver; PCR; primer; detection;  22 Cytochrome P450 2C19; human: liver; PCR; primer; detection;  23 Cytochrome P450 2C19; human: liver; PCR; primer; detection;  24 Cytochrome P450 2C19; human: liver; PCR; primer; detection;  25 Cytochrome P450 2C19; human: liver; PCR; primer; detection;  26 Cytochrome P450 2C19; human: liver; PCR; primer; detection;  27 Cytochrome P450 2C19; human: liver; |
|---|---|---|--|--|--|---|--|--|---|--|
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| CC in the presence of guanosine cofactor. The present sequence is human XX XX Sequence 1748 BP; 478 A; 419 C; 365 G; 486 T; 0 other; Cuery Match 1748 BP; 478 A; 419 C; 365 G; 486 T; 0 other; Cuery Match 1748; Score 1739, 6; DB 22; Length 1748; Best Local Similarity 99;81; Pred. No. 0; Matches 1742; Conservative 0; Mismatches 4; Indels 0; Gaps 0; | 1 ctccatggatcctttgtggtccttgtgtctctccatgtttgcttctctttcaa<br> | Oy b. tetagagacagagactetaggagagaaaateteeteeteegeeegeegeegeegee   Db 63 tetagagacagagactetgggagagaaaaeteeteeteegeeegeegee   Db 121 ttggaaatateetacagatagatataaagagateteeteeteeteeteeteegeegee   Oy 121 ttggaaatateetacagatagatataaagattetaagaaateetetaacaateeteea   Db 123 ttggaaatateetacagatatataaagattetaacaateeteea   Db 123 ttggaaatateetacaqataatataaaqatteaaqatattaacaateeteea   Db 123 ttggaaatateeteeaqatattaaaqatataaaqatateaaqaatataacaateeteea   Db 123 ttggaaatateeteeaqatattaaaqatateaaqaatataacaateeteea   Db 123 ttggaaatateetee | 181 anatctatggccctgtgttcactctgt<br>                                    | Db 243 gatafgaagragstgaagraacctggttgattgattgaggggttttttggaagaggc 302 Oy 301 atttcccactggctgaaagagctaacagaggatttggaacgttttcagcaatggaaaga 350 Db 303 atttcccactggctqaaagagctaacagaggatttgaatcgttttcagcaatggaaaga 352 Db 303 atttcccactggctqaaagagctaacagaggatttgaatcgttttcagcaatggaaaa 352 | 361 gatggaaggagattcggcgtttctccttatgacgctgcggaattttgggatgggaaga<br> | Oy         421 gqagcattgagaccgtgttcaaqagaagcccgctgccttgtggaagattgagaaaaa 480           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII | **************************************                 | Oy 601 aaaattgaatgaaacatcaggattgtaagcacccctggatccagatatcsatatt 550 | Oy 721 ttatggaaagtgatattttggagaaagtaaaagaacaccaagaatcgatggacatcaaca 780<br> | Oy 781 accetegggaetttattgattgettectgateaaatggagaaggaaaagcaaaccaac 840  |

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P450 2C19; human: liver; PCR; primer; detection;
.fic S-mephenytoin 4'-hydroxybame activity; polymorphism; ss.
                                                                                                          andard; cDNA; 1745 BP
                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                      P450 2C19 CDNA
1748
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421 421 601 601

6 % B

6 B 6

721 721 781

S ap

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This sequence encodes the cytochrome P450 2C19 and was isolated from a human liver cDNA library. 2C19 proteins exhibit stereospecific S-CC mephenytola decivity, with a typical activity of at least I much mephenytola per mol of 2C19 per min. 2C19 is thought to be the principal human determinant of this activity. The 2C19 is contains polymorphisms at nucleotides 616 and 681 of the genomic contains polymorphisms at nucleotides 616 and 681 of the genomic contains polymorphisms at nucleotides 616 and 681 of the genomic coling sequence. These can be detected using specific PKE primers which ether amplify the wild type or the mutant aliele but not both. These mutations cause the polypeptide to lack substantial S-CC both. These mutations cause the polypeptide to lack substantial S-CC individuals which lack S-mephenytolin 4 'hydroxylase activity, however the phenotype in most complete or substantial absence of 2C19 polypeptide.

2C19 can be used to identify drugs metabolised by S-mephenytolin C 4'-hydroxylase activity which should not be administered to individuals with a deficiency in S-mephenytoln 4' hydroxylase activity.
                                                                                                                                                                                                                                                                                                                                                                                                             New isolated cytochrome P450 2C subfamily member - used for identifying drugs metabolised by 5-mephonyoin 4'-hydroxylase activity and to develop other screening assays
                                                                                                                                                                                                                                                                                                             De Morais SMF, Goldstein JA, Romkes-Sparks M;
                                                     /*tag= a
/product= Cytochrome P450 2C19
                                                                                                                                                                                                                                                                     (USSH ) US DEPT HEALTH & HUMAN SERVICES.
Location/Qualifiers
6..1478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 92-93; 169pp; English.
                                                                                                                                                                                                                               9405-0238821.
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                                                                                                                                                                                                                                                                                                                                                  WPI: 1996-077257/08.
P-PSDB: AAR88329.
                                                                                                                                                                                                                             06-MAY-1994;
                                                                                                             W09530766-A1.
                                                                                                                                                                                       08-MAY-1995;
                                                                                                                                               16-NOV-1995.
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Sequence 1746 BP; 477 A; 417 C; 365 G; 487 T; 0 other.

| Ouer | Query Match 99.51; Score 1738; DB 17; Length 1746;                  |         |
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| Matc | ā   | :0<br>s |
| 6    | 1 cttcaatggatcettttgtgggteettgtgctctgtctctcatgtttgcttctcctttcaa 60  | 0       |
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| 8    |   | 300     |
| 윰    | 241 gatatgaagtggtgaaggaagccctgattgatcttggagaggagttttctggaagaggcc 36 | 300     |
| o,   | 301 atttcccactggctgaaagagctaacagaggatttggaatcgttttcagcaatggaaaga 36 | 350     |
| đ    | 301 atttcccactggctgaaagagctaacagagatttggaatcqttttcagcaatggaaga 350  | 90      |

1021 tocacquagqccacatgcctacaaqatqctqtqqtqaacqaqqtcaqqqaaaca 1080 1021 tycaqqacaqqqccacatgcctacacqqqtqtqqqqqqqqcacqqqqqtcaqqqqataca 1441 tecegecettetateagetgtgetteatteetgtetgaagaageaeagatggtetggetg 1500 781 901 901 8 3 B Q S G å q 6 G ö g ő õ ć ö C) ő g ć

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This sequence represents the wild type human liver derived cytochrome P450 ZC19 spee. Modified versions of the encoded protein are the proteins of the human Livention. The modifications comprise a substitution of the second mino acid with Ala and a deletion of amino acid residues 3-20 of the wild type. Modified cytochrome P450 ZC19 is useful for, uninterrupted metabolism of therapeutics, e.g. omegrazole, diazepam and imipramine in humans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18] amaictalgaccraigiteartcigtaittigactigaacgaatgatgatgatgcigcag 240
208 amaictalgaccgagiteactgaattigagctgaacgaatgaatgatggcigcag 267
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628 aaaattgaatgaaacatcaggattgtaagcacccctggatccagatatgcataatt 687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   388 gatggaaggagatccggcgtttctccctcatgacgctgcggaattttgggatggggaaga 447
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                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
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                                                                                                                                                                                                                                                         Sequence 1669 BP: 449 A: 405 C; 363 G; 452 T; 0 other;
      Claim 11; Page 11-12; 15pp; Japanese
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                                                                                                                                                                        Cytochrome P450 2C19; human; uninterrupted metabolism; omeprazole; diazepam; imipramine; ss.
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33..1505
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P-PSDB; AAW41161.
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cytochrome P450 protein. The fusion protein can oxidise hydrocarbons or any compound having a carbon-hydrogen boad. The fusion protein can be used for hydroxylating a compound to be oxidised. It can also be used in the bioremediation of an environmental pollutant. Since the fusion protein is soluble. It can be subject to structural elucidation by X-ray expressed in soil beateria to facilitate bloremediation. The present sequence encodes mammalian sytochrome PTSD protein CFP209 from the
                                                                                                                                                                                                                                                                                                                                                              invention describes a fusion proteins comprising a portion all cytochrome P450 protein and also a portion of a mammalian
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Pred. No. 0;
0; Mismatches 109; Indels 17; Gaps
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Best Local Similarity 92.9%;
Matches 1637; Conservative (
                                                                      98WO-0S16979
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                                                                                                                                                                                                                                                                                                                                                                                       cytochrome P450 protein.
                                                                                                                                      (UYRP ) UNIV ROCHESTER.
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P-PSDB; AAY04127.
                                                                    17-AUG-1998;
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                                                                                                                                                                                                                                 1048 tgcagacagggccacatgccctacacagatgctgtggtgcacagaggtccagagataca 1107
                                                                                                                                                                                                                                                                                                                                                                                                                                       tgcacgacaggggccacatgccctacacagatgctgtggtgcacgaggtccagagataca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalian cytochrome P450 protein CYP2C9 encoding DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAX19925 standard; DNA; 1845 BP
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| Db 1566 taatgcctttctcacctgtcatctccacatttcccttcccgaagatctagtgaacatt 1625 0y 1614 cagcctccattaababagtttcactgtgcaatatatctgctattccca 1661 1 | HIJ381 AAT11 AAT11 O9-SE Cytoc Cytoc Stere                             | D 16-NOV-1995.  F 08-MAY-1995; 95WO-US05744.  R 06-MAY-1994; 94US-0238821.  A (USSH ) US DEPT HEALTH & HUMAN SERVICES.  A (USSH ) US DEPT HEALTH & FOWENS-Sparks M:  De Morais SMF, Coldstein JA, Romkes-Sparks M:  R WPI: 1996-077257/08.  R P-PSDB: AAR89865.  X New isolated cytochrome P450 2C subfamily member - used for deartifular marabolised has emphasized by Correction A C - human and A C - human A | Example 2: Page 104: 169pp: English.  Example 2: Page 104: 169pp: English.  CC C H40 2C9. The majority of clones isolated from liver Si3 coded for 200 of the 50 clones encoding atted from liver Si3 coded for 200 of the 50 clones encoding 209, only two allelic variants were found.  CC Of the 50 clones encoding 209, only two allelic variants were found.  CC of the 50 clones ence identical with clone 55, and 11 were identical in the former 25. Clones 25 and 65 are identical in the 5' and 11 were demitted in the control of 1075 and 1142. One of these base changes was conservative but the other clones 290 and 60 difference at position 359, ille to Leu. The clones 290 and 60 difference at worst in the coding region.  The following the control of 194 by one nucleotide in the coding region.  The following the control of 194 by 5' innocoding region. |
|---|--|---|--|
| cttcatcctgggctgtgctcctgcaatggetc<br>tcgattataaagatcacaatttcttaacttgatgg<br>   | ttatogaaagtgatattituggagaaagtaaaagaacacaagaatcgatggacatcaaca 780 tinii | actediticeasiggacaaccatedateacticectecticity(states) 200 actediticeasiggacaaccatedateacticectecticity(states) 200 actediticeasiggacaaccatedateacticetigateacigacaaca 1205 actediticeasiceasicasiggattigaccitectigateacigateacidacaaca 1205 asgaatticeasiceasicasigattigaccitectigateacidacidacigatigatigatigatigatigatigatigateacidacidacidacidacidacidacidacidacidacid   | gattgacccaaggacttgacacaactcctgttgtcaatggattgcttctgggggattgacccaaggacctgacacaactcctgttgtcaatggattgcttctggggggtgggggggg  |

us-09-763-292-1.rng

905

901 cagagacaacaagcacaaccctgagatatgctctcttcttctctgctgaagcacccagagg 960 HIIII HIIIII HIIIIIIIII HIIIIIIIIIII 906 cagagagacaacaaccagagattatatcttcttcttcttcttgttgaagcaccagagg 965 catetgaatttaetattgaaagettggaaacaetgeagttgaettgttggagettgga EESULT AAV44157
11D AAV4
XX
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AC AAV4
XX
DI 06-O
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DE HUMA g ò ę ò g g & g qq ò SP O S G O.y oy oy ò Oy Oy Oy Oy g ,; ;; in the 3' and a polyademylation signal 21 bases from the poly.A tail. Clone 6b has an unsusully long 3. "noncoding region containing three possible polyademylation signals with no poly.A tail. The differences in the 3 mon-coding regions could represent alterate splicing, allelic variants, or possibly separate genes. These clones are designated as alielic variants of 2018 because they differ by only one base in the coding region. They are most similar to 209 (82% amino acid homology). agicigaailcactailgaaaactiggiaaicacigcagcigactiaciiggagciggga 900 121 tiggaaatatootacagatagtataaggatgicagcaaacoottacooaitotoca 180 116 tiggaaatacoboagtaggiatiaaggaacacagaaacoottacooaitocaa 185 126 tiggaaatooboagataggaataaggaacacagaaacoottacooaitocaa 185 | 11arity | 97.91; Score 1534.6; DB 17; Length 1852; Pred. No. 0; O; Conservative 0; Mismatches 109; Indels 17; Gaps Sequence 1852 BP; 514 A; 424 C; 380 G; 534 T; 0 other; Query Match Best Local Similarity Matches 1637; Conserval 121 426 181 486 241 546 601 909 199 999 721 726 ç 8 8 윱 5 윰 요 8 셤 ð 8 & 8 8 3 5 8 5 중 중 윰 δ 윰 ç 윰 5 윰 ò Š 88888888

CDNA. Human cytochrome P450 2C9 clone 65 AAV44157 standard: cDNA: 1852 BP 06-OCT-1998 (first entry) AAV44157;

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601 gaagattgaatgaagacatcaggattgtaagcacccctggatccagatatgcaataatt 660
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                                                                                                                                                                                                Screening for drugs metabolised by cytochrome P450 - for identifying mutagenic, carcinogenic, or cytotoxic compounds
            Cytochrome P450; drug screening; S-mephenytoin 4'-hydroxylase; : identification; mutagenic; carcinogenic; cytotoxic; haemoprotein; recobiotic; environmental poliutant; ss.
                                                                                                                                                                                                                                                                                                                   Sequence 1852 BP; 514 A; 424 C; 380 G; 534 T; 0 other;
                                                                                                                                                                                                                          Example 2; Column 53-56; 63pp; English.
                                                                                                                                                                  Goldstein JA, Romkes-sparks
                                                                                                             94US-0201118.
92US-0864962.
                                                                                                94US-0201118
                                                                                                                                        (GOLD/) GOLDSTEIN J A. (ROME/) ROMEES-SPARKS H.
                                                                                                                                                                                 WPI; 1998-436528/37.
                                                                                                               22-FEB-1994;
09-APR-1992;
                                              Homo saplens.
                                                                                              22-FEB-1994;
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ò qq ò g ò q 0.7 qq õ a o, g ; **341 gatatgaagtggtgaaggaagccctgattgatcttggagaggagttttctggaagagcc 300** 301 attroccactggctgaagagctaacagaggatttggaatcgttttcagcaatggaaaga 360 246 gatatgaagcagtgaaggaagccctgattgatcttggagaggagttttctggaagaggca 305 421 ggagcattgaggaccgtgttcaagaggaagcccgctgccttgtggaggagttgagaaaa 480 1 ctrcaatggatccttttgtggtccttgtgctctgtctctccattga 60 Ouery Match 87.94; Score 1534.6; DB 19: Length 1852; Best Locas Similarity 92.94; Pred. No. 0; Matches 1637; Conservative 0; Mismatches 109; Indels 17: Gaps 6 ctrcaatggattctcttgtggtccttgtgctctgtctctcatgtttgcttctcttcac 65

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1501 ctcctgfgctgtccctgcagctctttcctctgg------tccaaatttcactatctg 1553 1081 tcgacctcatccccaccagcctgcccatgcagtgacctgtgacgttaaattcagaaact 1140 g ò

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results in one amino acid difference at position 359, lle to Leu. The clones 20c and 6b differ by one nucleotide in the coding region, position 1154, which results in a single amino acid change. Thi to Met at position 185. Clone 250 has a very long, 188 bp. 5-noncoding region and a polyadeuplation signal 21 bases from the poly. A tail. Clone 6b has an unusually long 7-noncoding region containing three possible polyadeuplation signals with no poly. A tail. The differences in the 3 non-coding regions could represent alterante splicing, allell c variants or possibly separate genes. These clones are designated as alleller variants of 2018 because they differ by only one base in the acoding region could make they differ by only one base in the acid homology).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     421 gaagcattaaggaccgtgttcaagagaaacccgttgccttgtgaagagttgagaaaaa 480
428 gaagcattaggaccgtgttcaagagaagccgttgcttgtgagagagttgagaaaa 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            661 ttcccactatcattqattattcccqqqaacccataacaaattacttaaaaaccttqctt 720
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                                                                                                                                                                                                                                                                                                                                                                               112; Indels 17; Gaps
                                                                                                                                                                                                                                                                                                         DB 17; Length 1854;
                                                                                                                                                                                                                                                  Sequence 1854 BP; 513 A; 424 C; 381 G; 536 T; 0 other;
                                                                                                                                                                                                                                                                                                         87.6%; Score 1529.8;
92.7%; Pred. No. 0;
sive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cytochrome P450 2C19; human; liver; PCR; primer; detection: CYP2C19; stereospecific S-mephenytoin 4'-hydroxylase activity; polymorphism: ss.
                                          1554 tgatgettettetgaccejeatetaaattitecetteeceaagatetagtaacast 1613
1566 taaggeettiteteecetjaatetaattiteetteeetgaaattijijii 1725
1866 taaggeettiteteeeetgaatetaattieetteeetgaagatetagtgaacat 1525
                                                                                                                  ctgctgtgcagtccctgcagctctctttcctctgggggcattatccatctttcactatctg 1565
                                                                                                                                                                                           1664 tactetataatagttacattgagtgecacataatgetgataettgtetaatgttgagtta 1723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mew isolated cytochrome P450 2C subfamily member - used for identifying drugs metabolised by S-mephenytoin 4'-hydroxylase activity and to develop other screening assays
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/product= Cytochrome P450 C9 clone 25
1087
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ote "Variable position"
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/note- "Variable position"
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13..1485
                                                                                                                                                                                                                                                                      BP.
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                                                                                                                                                                                                                                                                                                                                                                                                     AA-11378 standard; cDNA: 1854
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Cricohrome P450; drug screening: S-mephenytoin 4f-hydroxylase: 
Tednification: mutaqenic: carringqenic: cytotoxic; haemoprotein: 
xenobiotic; environmental pollutant; ss.
                                                                                   Human cytochrome P450 2C9 clone 25 cDNA.
                                06-OCT-1998 (first entry)
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05-APR-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1554 tgatgetretrergaccegicalcreacatticcettececeaagaictagigaacait 1613 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 
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AAV4154
ID AAV44154 standard; CDNA; 1854 BP.
XX AAV44154:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence encodes a cytochrome P450 2C9 polypeptide isolated from than clone 25. This polypeptide is used in a method to screen for a drug that is metabolised by a cytochrome P450 having S-mephenytoin P4. The protein can also be used to identify a mutagenic, carcinogenic or cytochrome also be used to identify a mutagenic, carcinogenic or cytochat compound. Cytochrome P450 are a large family of haemoprotein enzymes capable of metabolising xenobiotics enchas carcinogens and environmental pollutants as well as endoblotics such as steroids, fatty acids and prostaglandins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       211 gatatgaagtgatgaaggaagccctgattgatcttggagaggagtttctggaaagagcc 300
218 gatatgaagaggaggaaggaagcccgattgatcttgaagaggagtttctuggaaggagca 307
218 gatatgaagaggaaggaaggagccgattgatcttgaagaggagttttctuggaagagca 307
                                                                                                                                                                                                                                                                                                                                Screening for drugs metabolised by cytochrome P450 - for identifying mutagenic, carcinogenic, or cytotoxic compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87.6%; Score 1529.8; DB 19; Length 1854;
92.7%; Pred. No. 0;
Live 0; Mismatches 112; Indels 17; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1854 BP; 513 A; 424 C: 381 G; 536 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                             Example 2; Column 39-42; 63pp; English.
                                                                                                                                                                                                                     Coldstein JA, Romkes sparks M;
94US-0201118.
                                               94US-0201118
92US-0864962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 92.71
Matches 1634; Conservative
                                                                                                                                (GOLD/) GOLDSTEIN J A. (ROMK/) ROMKES-SPARKS M.
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gatggaaggagattcggcgtttctccctcatgacgctqcggaattttgggatgqgaaga 420

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| Db 1448 tgccgcccttctaccagctgtgcttcattcctgtctgaagaagagcagatggcctggtg 1507 Ou 1501 propertional pagent 1553 | 1   | 1560 taatoctictictgaccogicatotecaritticccticcccaagatotagigaacait        | UY 1614 cacciccated  | 1664                              | UY 1/24 Ctacostattattaantaga 1/45<br>                                   | RESULT 10<br>AAQ87728<br>ID AAQ87728 standard: CDNA: 1473 BP.           | AC AAO87728:<br>T 15-WOV-1995 (first entry)                                   |  | nument vycolinger volver amptation from planet, captession great MADHF-P150 reductase; safety; fusion protein, metabolite carcinogen; mutagen; liver metabolism; ds. | XX EP644267-A.<br>XX 22-HAR-1995.                                      | 20-JUL-1994;<br>21-JUL-1993;  | 20-JUL-1993; 93JP-02<br>30-JUL-1993; 93JP-02<br>(HAYA/) HAYASHI K. | ry (sumo ) sumilumo chem co Lib.<br>XX<br>PI Hayashi K, Kaneko H, Komai K, Nakatsuka I, Sakaki T:<br>PI Yabusaki Y; | WPI; 1995-1<br>P-PSDB; AAF  | PT Evaluation of safety of a chemical cpd using recombinant yeast PT expressing human cytochrome p450 and a yeast NADPH-P450 reductase XX Examples; Page 78-80; 124pp: English. |   | CC PAMBAN OF ANY AND ANY   |  |
|---|---|---|--|-----------------------------------|---|---|---|--|--|--|---|--|---|---|---|---|--|--|
|   | 421 ggagcattgaggaccgfgttcaagaggaagcccgctgccttgfggaggagttgagaaaa 480<br> | 481 ccaaggetteacctgtgateccacttteatectgggetgtgetecctgeaatgtgatet 540<br> | 541 getecatratiticcagaaacgiticcgattataaagatcacgaatticttaactigatgg 600 [hillin] [hill | aamaattgaatgaaaacatcaggattgta<br> | 661 ttcccactatcattgattattcccgggaacccataacaaattacttaaaaaccttgctt 720<br> | 721 ttatggaaagtgatattttggagaagtaaaagaacaccaagaatcgatggacatcaaca 780<br> | 781 accetcaggactitatigatigeticetgateaanatggagaaggaaageaaneeaee 840<br>   -  - | 841 agtotgaattoactatgaaaacttggtaatcactgcagctgacttacttggagctggg 900 | Cagagacaacagcacaaccagatatgctccctcccgcgagagaga  | 961 toacagotaaagtocaggaagattgaacgtgtcattggcagaaaccggagccctgca 1020<br> | 1021 tgcacgacaggggccacatgcctacacagatgctgtggtgcacgaggtccagagataca 1080 | togacctcatcccaccagcctgcccatgcagtgacctgtgacgttaaattcagaaact         | 141 acctcattcccaagggcacaaccatattaacttccctcacttctgcctacatgacaaca 1200  | 1201 aagaatttoccaacccagagatgttgaccctgtcactttctggatgaaggtggaatt 1260 |   | 1331 gectggccgcatggagctgttttattcctgaccttcatttacagaactttaacctga 1380<br> | aatctctgaltgacccaaaggaccttgacacaactcctgttgtcaatgatttgttttg<br> |  |

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| through metabolism in the liver.  Sequence 1473 BF: 404 A: 35 C; 327 G; 390 T; 0 other;  Sequence 1473 BF: 404 A: 35 C; 327 G; 390 T; 0 other;  Sequence 1473 BF: 404 A: 35 C; 327 G; 390 T; 0 other;  Best Local Similarity 99.4; Pred. Mo. 0;  Marches 146; Conservative; Pred. Mo. 0;  Retches 146; Conservative; G: Mismatches 9; Indels 0: Gaps 0: Inilinity | 996 gectaagtecaggaaggattgaacqtgtcattggcagaaaccggagccctgcatgcac 1025   |
|---|---|
| Score 1458.6: De 16: Length 1473: Fred. No. 0; 0: Mismatches 9: Indels 0: Gaps O: Mismatches 11   O: Mismatches 12  | 961 gitaáagiccaggaagagatigaacgidicgitigcagaaaccggaaccctgcatgaag<br>1026 gacaggggcacatacctcacacagatcgtggrgcagaagggccagagtcactgaa<br>101 gacaggggcacatgccctacacagatcgtggrgcagagggccagagtccagagatcatcgac<br>1086 ctcatccccaccagcctgcccagagacctgtgggggcgagggcacagagatacatcgac<br>1086 ctcatccccaccagcctgcccagagagacctgtgacgttaaattcagaaactacctc<br>1186 attcccaagggcacaaccatattaacttccctcacttctggactaatacagacaacaaagaa<br>1186 attcccaagggcacaaccatattaacttccctcacttctggactaatacaagaaaatacctc<br>1186 attcccaagggcacaaccatattaacttccctcacttctggacaagacaacaaagaa<br>1206 tttcccaaccaagggacaaccatttaacttccctcacttctggataaatgacaacaaagaa<br>1206 tttcccaaccaaggacaacacttcattgacctcgtcacttctggatgaaggggaaaattttaag<br>1207 ttccccaacccaaggagatttgacctcgtcacttctggatgaaggggagaagagggcctg<br>1181 |
| Score 1458.6: DB 16: Length 1473: Pred. No. 0: 0: Mismatches 9: Indels 0: Gaps 0: Mismatches 9: Indels 0: Gaps creditercengtitectrecetteacterg 65   | 1026 gacaggggccacatgccctecacaggtggtggacgggggggggtcacaggatcatcgacalin  |
| getctgtctctatgtttgcttctctttcaatctgg   | 1086 ctcatecceagectgecraceageageactgeagetteaateacectc   |
|   |   |
|   | 1206 tttcccaaccaaqaqqtqtqqcccqccacttcqqqatqaqqqqqaaatttaaq<br>1201 ttcccaaccaaqaqqtqttqqccctqqtcactttcqqatqaaqqqqaaattttaaq<br>1266 aaaaqtaactacttcatqcctttctcaqcaqqaaaqqqqqqqq   |
|   | 1266 aaaaqtaactacttcaqccaqcaqaaaaqqatttqtqqqaaaqqcctq 1261 aaaaqtaactacttcaqcqqqaaaaqqcctq 1261 aaaaqaaactacttcaqccqqqaaaaqqqqqqqqqqqqq   |
| ttggcctcgagggcatggtgtgctgcatggatat<br>ttcttggagaggagtttctggaagaggccatttc<br>  | 1326 geoegeatggagetgttttatteetgacetteatttacagaaetttaacetgaaatet<br>   |
|   |   |
| <pre>gaagtggtgaaggaagccctgattgatcttggagaggagttttctggaagagccatttc 300 ccactggctgaaagagctaacagagatttggaatcgttttcagcaatggaaagagatgg 355 HIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII</pre>   | Oy 1386 ctgattgacccaaaggaccttgacacaactcctgttgtcaatggattgcttctgtcccg 1445  |
| gartegyaaregriikaagaagagagaga<br>tgacgetyeggaatttiggatgggagggaagagag<br>tgacgetyeggaattttegggatgggaagagag<br>tgacgetygaattttegggatgggaagagaga   | Oy 1446 coettetateagetgttettectgtetga 1478  |
| attgaggaccgtgttcaagaggaagcccgctgccttgtgaggagttgagaaaaaccaag 485<br>   | RESULT 11<br>AA128394<br>ID AA728394 standard; DNA; 1473 BP.  |
| <pre>gcttcaccctgtgatcccactttcatcctgggctgtgctccctgcaatgtgatctgctcc 545                                    </pre>   | XX AAT28394;<br>XX II-OCT-1996 (first entry)  |
|   | Human cytochrome P450 molecular species 2C19 gene.  |
|   | KW Human Cytochrome P450; amplified; PCR; polymerase chain reaction; primer KW liver; yeast; expression vector; NAPH-P450 reductase; ABH gene promoter KW evaluation; safety; fusion protein; metabolite; detoxification; KW carcinogenic; ds. XX   |
| ccataacaaattacttaaaaaaccttgcttttatg   | OS Homo saptens.<br>XX XX YF U JP08056695.A.  |
| activity yydaa tota aa a   | PD 05-MAR-1996.<br>XX X PF 15-JUL-1994; 94JP-0164184.   |
| <pre>gaaagtgatattttggagaaagtaaaagaacaccaagaatcgatggacatcaacaacccc cgggactttattgattgcttcctgatcaaaatggagaaaggaaaagcaaaaccaacaftct lllllllllllllllllllllllllllllllllll</pre>   | AX 17-JUN-1994; 94.JP-0136053.<br>PR 20-JUL-1993; 93.JP-0201120.<br>PR 30-JUL-1993; 93.JP-0208279.  |
| gastcactattgaaaacttgtaatcactgcagctactacttgagctggacagagallillillillillillillillillillillillilli  | PA (SUMO ) SUMITOMO CHEM CO LID.  XX  XX  DX HP1; 1995-182311/19.  DR P-PSDB: AAR93181.   |
| 121 21 21 21 21 21 21 21 21 21 21 21 21   | cccgctgccttgtggaggttggagaaaaccaag tcctgggctgtgctcctgcaatgtatctgtcc tctgggctggctccctgcaatgtgatctgtcc tctgggctggctccctgcaatgtgatctgctcc ataaagatcacgaattcttaacttgatggaaaa filiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiii   |

450; amplified; PCR; polymerase chain reaction; primer: ession vector; NADRH-4450; reductase; ADR quee promoter: (asion protein; metabolite; deloxification; 450 molecular species 2019 gene. HEM CO LID. JP-0136053. JP-0201120. JP-0208279. P-0164184 t entry)

actateattgattattcccgggaacccataacaattacttaaaaccttgctttatg 725

661 726 721

999

g

Novel method for the evaluation of the safety of a cpd. - using a binam cytochrome P450 and yeast MADPH reductase to determine whether the analyte cpd. is detoxified or metabolised to a carcinogen Example 1; Page 47-49; 74pp; Japanese.

This is the nucleotide sequence of the human cytochrome Pi50 molecular species 2019 gene which encodes a protein of 400 amino acids. The gene species 2019 gene which encodes a protein of 400 amino acids. The gene consists and itself from a human liver derived cDNA library as several consists amplitied from a human liver derived cDNA library as several consists and library as several consists. The prod. was cloned into the formation of the cytochrome only or into the vector pANRA to generate plasmid pacing for corprod. With the yeast ADNPH Ph50 reductase the plasmid paced under control of the yeast ADNPH Ph50 reductase. The sequence is placed under control of the yeast ADNPH produced human cytochrome Ph50 call the test cpd. With recombinantly produced human cytochrome Ph50 call their section their variants (AAT2888), 25 (AAAT2888), 22 (AAAT2888), 22 (AAAT2888), 22 (AAAT2888), 22 (AAAT2888), 22 (AAAT2888), 23 (AAAT2888), 23 (AAAT2888), 24 (AAAT2888), 24 (AAAT2888), 25 (AAAT2888), 25

Query Match
Best Local Similarity 99.44; Pred. No. 0;
Matches 1464; Conservative 0; Mismatches 9; Indels 0; Gaps 0

1440 Saccharomyces cerevisiae: 1446 continuation of the state Human liver cytochrome P-450 encoding gene. AAQ03599 standard: DNA: 1818 03-SEP-1990 (first entry) P-450; cytochrome: liver disorders; ds Homo sapiens AA003599; PESULT 12 AA003599 1205 1201 1386 1381 QQ QQ ò g ò 6 g ò Ş 8 g ò ő ò Ω οy õ g ò a

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The P-450 produced from plasmid phPA6 in a yeast expression system referably Secrebranowees ANI2, can be used to treat human liver disorders, oxidising various chemical substances.
                                                                                                                                                                                                                                                                                                                                                                         Recombinant plasmid, for yeast for liver treatment -
comprises human liver cytochrome P-450MP gene obtd. from yeast,
etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1818 BP; 516 A; 412 C; 376 G; 514 T; 0 other;
Location/Qualifiers
1..1443
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 4: 9pp; Japanese.
                                                                                                                                                                                                                                                                            (AGEN ) AGENCY OF IND SCI TECH.
                                                                                                                                                                                                                                09-SEP-1988; 88JP-0225955.
                                                                                                                                                                                 09-SEP-1988; 88JP-0225955.
                                                                                                                                                                                                                                                                                                                       WPI; 1990-121045/16.
P-PSDB; AAR04043.
                                                                                          JP02072879-A.
                                                                                                                                      13-MAR-1990.
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| i di       | Query Katch   | rb 83 38. Score 1455; DR 11: Length 1818;  | Oy           | 1077 t      |
|------------|---------------|--|--------------|-------------|
| Best       | 100           | Similarity 92.2%; Pred. No. 0.   | qq           | 1045 t      |
| 2          |               | ייי שומות רווים אורי אותפוים איי פולים איי פולים פ | Oy           | 1137 a      |
| Š          |               |  | a            | 1105 a      |
| g          |               |  | ٥y           | 1197 a      |
| ሯ          | 117 g<br>     | gtgattggaaatatCctacagatagtattaaggatgtcagcaaatccttaaccaatctc 176  | q            | 1165 a      |
| a          | 91 9          | gigatiggaaatateetacagataggtattaaggacateageaaateettaaceaatete 150   | ò            | 1257 a      |
| ð          | 177 t         | tcaaaaatctatggccctgtgttcactctgtattttggcctggaacgcatggtgctg 236  | - 8          | 1<br>1225 a |
| a          | 151 t         | tcamaggictatggcccggtgttcactctgtattttggcctgaaacccatagtggtgctg 210   | ě            | 1317 0      |
| ð          | 237 C         | catggatatgaagtggtgaaggaagccctgattgatcttggagaggagttttctggaaga 296   | <b>7</b> 1   |             |
| £          | - [[          |  | e<br>S       | 1285 9      |
| 3          |               |  | o,           | 1377 C      |
| ď          | 297 9         | ggccatttcccactggctgaaagagctaacagaggatttggaatcgttttcagcaatgga 356   | ć            | 1345        |
| ag         | 271 q         |  | 3            |             |
| !          |               |  | oy           | 1437 t      |
| ģ          | 357 a         | aagagatggaaggagattcggcgtttctccctcatgacgctgcggaatttgggatgggg 415<br>  | q            | 1405 t      |
| 윮          | 331 8         | aagaaatggaaggagatccggcgtttctccctcatgacgctgcggaattttgggatgggg 390   | ě            | 1407        |
| 5          | 417.0         | agaagaarattaagaarcatotteaagaagacccoctoccttotogaagattgaga 475   | ŝ            | Ď (6•1      |
| ;          |               |  | đ            | 1465 9      |
| 8          | 331 a         | aagaggagcattgaggaccgtgttcaagaggaagcccgctgccttgtggaaggagttgaga 450  | oy           | 1550 t      |
| 04         | 477 8         | aaaaccaaggetteaccetgtgateceaettteateetgggetgtgeteeetgeaatgtg 536   | đ            | 1525 t      |
| 8          | <b>4</b> 51 a | aaaaccaaggcctcaccctgtgatcccactttcatcctgggctgtgctccctgcaatgtg 510   | è            | 0.01        |
| 8          | 537           | atetoricatiatiticagaaacditicgattataaagatcacgaatticttaacttg 596   | Š            | -           |
| <b>3</b> 1 |               |  | <del>g</del> | 1585 c      |
| 8          | 511 8         | atctgetecattatttecataaaegitttgattataaagateageaatttettaaetta 570  | ò            | 1660 0      |
| ģ          | 597 8         | atggaadaattgaatgaaaacatcaggattgtaagcacccctggatccagatatgcaat 555  | É            | 1645        |
| 8          | 571 8         | atggaaaagttgaatgaaaaacatcaagattttgagcagcccctggatccagatctgcaat 630  | ì            |             |
|            |               |  |              |             |

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218 aagtetatggeeetgtgtteaetnigtattttggeetgaaaceeatagtggtgnigeaig 277
                                                           241 gataigaagtggtgaaggaagccctgattgatcttggagagaggittctggaagagcc 300
278 gattgaaggagggaggaaggagccctgattgatcnggagagagggttttcttggaagagco 337
                                                                                                                                                                                          30] atticccactgcctgaaagagctaacagagattiggaatcgtticgcaatggaaga 360
338 htticccattgctgaagagataacaaggantiggaatcgtticagcaatggaaga 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               this sequence encodes a human cytochrome P450 2C polypeptide. This by veptide is used in a method too screen for a drug that is methodised by a cytochrome P450 having S-mephenytoin 4' hydroxylase activity. The protein can also be used to identify a muteponic, carcinogenic or cytotean compound. Cytochrome P450 are a large family of haemoprotein enzymes capable of metabolising xenoblotics such as drugs carcinogens and enzionmental pollutants as well as endoblotics such as steroids, fatty acids and prostaglandins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Screening for drugs metabolised by cytochrome P450 - for identifying mutagemic, carcinogemic, or cytotoxic compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cytochrome P450; drug screening; S-mephenytoin 4'-hydroxylase:
Identification: mutagenic carcinogenic; cytotoxic; haemoprotein:
xenobiotic; environmental pollutant; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1892 BP; 481 A; 396 C; 358 G; 500 T; 157 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Column 63-66; 63pp; English.
        Human cytochrome P450 2C genomic DNA
                                                                                                                                                                                                                                AAV44159 standard; DNA; 1892 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Goldstein JA, Romkes-sparks M;
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92US-0864962
                                                                                                                                                                                                                                                                                                                                                           06-0CT-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GOLD/) GOLDSTEIN J A. (ROMK/) ROMKES-SPARKS M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1998-436528/37.
P-PSDB; AAW64075.
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09-APR-1992;
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ANA 41159

ID ANA 41151

ID ANA 4
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1201 aagaattteceaacceagagatgtttgaccetegteacttetggatgaaagtggaaatt 1260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           721 ttatggaaagtgatattttggagaaagtaaaagsacaccaagaatcgatggacatcaaca 780
758 ttatgaaagtalttttggagaaagtaaaagaacaccaagaatcantggacatgaaca 817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48] ccaaggettcaccetg.catccacttcatcctgggctgtgctccctgcaargtgatct 540 [III] [III]
                                                                                                                                                                                                                                 ggagcattgaggaccgtqttcaagaggaagcccgctgccttgtggaggagttgagaaaaa 517
                                                                                                                                                                                                                                                                                                                                                                                              601 aaaaattgaatgaaacatcaggattgtaagcacccctggatccagatatgcaataatt 660
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Ouery Match 82.31; Score 1436.4; DB 19; Length 1892; Best Local Similarity 86.31; Pred. No. 0; Matches 1523; Conservative 0; Mismatches 221; Indels 17; Gaps

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ξ 윱 Š 181 aaatctatggccctgtgttcactctgtattttggcctggaacgcatggtggtgctgcatg 240

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ctcttgtgtgttgtcctgcagetcttttctttgg.....tccaaatttcactatctg 1553
                                                                                                                                                                                                                                                                                                                                                                                                                             nannuncaatntccaagagngtgnntttnttnnctntccacctanatctatcnntnnnc 1717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is a genetic construct for bacterial production of a cytochydme P450 monoxygenase. The invention relates to a method for producing plyment Wing cells containing cytochrome P450 sequences it involves the use of genetic material encoding a cytochrome P450
1614 cagcetecattaaaaa.....agttteactgtgcaaatatatetgetatteeeca 1563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1664 tactetataatagttacattgagtgecacataatgetgataettgtetaatgttgagtta 1723
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Generation of genetically modified cell to produce pigment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genetic construct for bacterial production of P450 2C19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human: cytochrome P450 2C19 monooxygenase; P450 2C19;
pigment production; indole; dye; cosmetic industry; m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 11; Page 164-168; 178pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UTQU ) UNIV QUEENSLAND.
(UTVA-) UNIV VANDERBILI.
(CALT ) CALIFORNIA INST OF TECHNOLOGY.
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                                                           1358
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AAPT 5564
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AAPT 5664

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of it in the generation
e capacity to produce a
                              pigment in the presence of indole, or a precursor, analogue or derivative of indole, upon expression of the genetic material. Pigment from plant or plant material is useful in the dye or cosmetto industry or as commercial tags or as markers for transformation of microbial, plant or animal cells.
                                                                                                                                                                                                                                                                                                                                                                 247 aagtgatgaaggcctgattgatcttgaagaggagttttctggaagaggccatttcc 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cttcaccctgtgatcccactttcatcctggctgtgctccctgcaatgtgatctgctcca 546
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            667 ctatcaligatiatitocoggaaccolaacaaattacitaaaaacciiociitiaigg 726
608 tiatcaligatiaticooggaaccolaacaaattacitaaaacciigciitiigg 667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gggactttattgattgcttcctgatcaaalggagaaggaaaaggaaaagcaaaagtctg 846
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788 aattoacttgaaaacttggtaatcactgoagctgactacttggagctgggacagaga 847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             caacaaccacaacccigagalatgctctccttctcctgctgaagcacccagaggtcacag 966
                                                                                                                                                                                                                                      127 atatectacagatagatattaaggatgteagcaaateettaaceaateteteaaaaatet 186
                                                                                                                                                                                                                                                                                                                          188 aagtggtgaaggaagccctgattgatcttggaggaagttttctggaagaagccatttcc 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cactggctgaaagagctaacagaggattdgaatcgtttcagcaatggaaagagatgga 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   367 aggagatteggegttececeatgaegetgeggaatttegggatggggaagaga 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    428 etteaccetgigateceaettteateciggetgigetecetgeaatgigatetgeteea 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       547 ttattttccagaaacgtttcgattataaagatcacgaatttcttaacttgatggaaaat 606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           aaagtgatattttggagaaagtaaaagaacaccaagaatcgatggacatcaacaacctc 786
                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                         DB 22; Length 8475;
                                                                                                                           Sequence 8475 BP; 2042 A; 2237 C; 2215 G; 1981 T; 0 other;
                                                                                                                                                                         Score 1415.2; DB 22; Lengt
Pred. No. 0;
0; Mismatches 18; Indels
  or
                                                                                                                                                                         Query Match 81.1
Best Local Similarity 98.8
Matches 1426; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             307
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307 cactgoctaaaagagctaacagagatttggaatcgttttcggcaatggaaagagtgga 366
251 cactgottaaaagagctaacagaggatttggaatcgttttcggcaatggaaagagaga 310
                                                                                                                                     Claim 4; Page 9-10; 15pp; Japanese
                            96JP-0193015.
                      96JP-0193015
                                  (SHIO ) SHIONOGI & CO LID.
                                        WPI: 1998-172087/16.
P-PSDB: AAW41160.
                     23-JUL-1996;
                            23-JUL-1996;
         JP10033166-A.
               10-FEB-1998.
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                                                                                caacaagcacaacctgagatatgctctccttctctgaagcacccagaggtcacag 907
                                                                                                                                                                     Cytochrome P450 2C19; human; uninterrupted metabolism; omeprazole; diazepam; imipramine; mutein; ss.
      aa: Asn)
                                                                                                                                                                                    Cytochrome P450 2C19 mutein gene.
                                                                                                                                             AAV12758 standard; cDNA; 1447 BP
                                                                                                                                                          08-MAY-1998 (first entry)
                                                                                                                       1507 tgct 1510
                                                                                                                             1448 gtct 1451
                                                                                                                                                                                Homo sapiens.
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                  1027
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This sequence represents the modified version of the human liver derived vyclornom pt 950 ZL19 gene of the invention. The modifications comprise a substitution of the second amino acid with Ala and a deletion of amino acid vith Ala and a deletion of amino acid residues 3.20 of the wild type. Modified cytochrome pt.90 ZC19 is useful for, uninterrupted metabolism of therapeutics, e.g. omeprazole, diazepam and imipramine in humans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 81.0%; Score 1413.6; DB 19; Length 1447; Best Local Similarity 99.0%; Pred. No. 0; Matches 1422; Conservative 0; Hismatches 14; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified cytochrome P450 2019 from human liver - useful for uninterrupted metabolism of therapeutics, e.g. omeprazole
/transl_except= (pos: 1306..1308, aa:Asn)
/transl_except= (pos: 1396..1398, aa:Asn)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1447 BP; 410 A; 341 C; 322 G; 374 T; 0 other;
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| 5 8    |   | arrarrrecededaacecaraacaaarraecraaaaaacerroorrraraa                   | 126          |
|--------|---|---|--------------|
| 3      | cattg   |   |              |
| ÷ 8    | 727 aaagtgata                                 | tgarattitgagaaagtaaagacaccaagaatgaatgacatcaacacctt 7                  | 186          |
|        |   |   | 130          |
| 6 6    | 787 gggactta                                  | ttgattgcttcctgatcaaatggagaaggaaagcaaaaccaacagtctg 8                   | 345          |
|        |   |   | 190          |
| 6 G    | 847 aattcacta                                 | <b>ttcactaitgaaaa</b> ctiggiaatcactgcagctgacttactiggagciggacaaaa 9    | 505          |
|        |   |   | 350          |
| 5 B    | 907 caacaagca                                 | caagcacaacctgagatatgctctcttctctgtgaagcacccagagtcacag 9                | 966          |
|        |   |   | 910          |
| රු පු  | 967 ctaaagtcc<br>                             | ctaaagtocaggaagattgaacgtgtcattggcagaaaccggagcccttgcatgca              | 1025<br>970  |
| Oy 1   | 027 acaggggccac                               | atgccctacacagatgctgtgtgtgcacgaggtccagagatacatcgacc                    | 1085         |
|        |   |   | 1030         |
| 0y 1   | 087 tcatcccca<br>                             | tcatcoccaccagctyccccatgcagtgactytgacgttaaattcagaaactactca 1<br>       | 1146         |
| 1 de 1 | 1147 ttcccaaggcac                             | aaccatattaacttccctcacttctgtgctacatgacaacaaagaat                       | 1206         |
|        |   |   | 1150         |
| 1 B    | 1207 ttcccaacc<br>         <br> 151 ttcccaacc | ttcccaacccagagatgtttgaccttgtcactttctggatgaaggtggaattttaaga  <br>      | 1266<br>1210 |
| B 3    | 267 aaagtaact                                 | <b>aaaytaactacttcotgcctttctc</b> agcaggaaaacggatttgtytgggagaggcctgg 1 | 1326         |
|        |   |   | 1270         |
| 8 6    | 327 cccgcatgg<br>                             | 0 - 0   | 1386<br>1330 |
| 9 J    | 387 tgattgacc                                 | gatigacccaaagacctigacacaciccigiigicaatgatiigciicigiccgc               | 1 <b>446</b> |
|        |   |   | 1390         |
| 99     | 447 cettetate                                 | cettetateagetgigetteatteetgetgaagaageaeagatggietggetget 1502          |              |
| 11     |   |   |              |

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| 13 589.8   33.8   907   11   BC205076   BC205076   BC205076   BC116520   BC1166022   BC1166024   BC116604     | RESULT 1  AKO08580 1990 bp MRNA HTC 05-JUL-2001  DEFINITION MS misculus adult male small intestine CDNA, RIKEN full-length enriched library, clone:201018706, full insert sequence.  ACCESSION VERSION AKO08580 1990 bp MRNA HTC 05-JUL-2001  VERSION AKO08590.1 GT:1284282  CAP tipper. Strain:C57HL/6) adult male small intestine CDNA to mRNA, clone_11b, ERENEM full-length enriched mouse CDNA library clone:201018066.  ANTHORS MANA CLONE_10018066.  ANTHORS Carninci,P. and Haysbilzaki,Y. Hille High-efficiency full-length CDNA clonein Huse.  High-efficiency full-length CDNA cloning Muridae: Murinae; Mus. High-efficiency full-length CDNA cloning Mussalizaki,Y.  REFERENCE HUSE CARNOW, W. OARSANIY, W. and Haysbilzaki,Y.  REFRENCE CARNOW, W. OARSANIY, W. Haysbilzaki,Y.  High-efficiency full-length CDNA cloning Mussalizaki,Y.  NOTHALIZE HORD, W. Shibata,Y. Haysbilan, W. and Haysbilzaki,Y.  NOTHALIZE LICAPA, K. STANIN, CARNOW, W. CARNOW, W. OARSANIY, W. HAYSBILZEN, CARNOW, W. OARSANIY, W. NOTHABALE, W. NASHINE, Y. NOTHABALE, W. NASHINE, Y. NOTHABALE, W. NASHINE, Y. SHIBALE, W. NASHINE, Y. SHIBALE, W. NASHINE, Y. SHIBALE, W. NASHINE, Y. NASHINE, W. SHIBALE, W. NASHINE, Y. HAYBALE, W. NASHINE, Y. NASHINE, Y. SHANDAL, W. CHANDAL, W. OABBALE, W. OABBALE, W. WASHINE, W. OABBALE, W. WASHINE, W. WASHINE, Y. HAYBALE, W. WASHINE, Y. HAYBALE, W. WASHINE, W. OABBALE, W. WASHINE, W. OABBALE, W. WASHINE, |
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| Copyright (c) 1993 - 2000 Compugen Ltd.  CM nucleic - nucleic search, using sw model  Run on: April 19, 2002, 07:21:40; Search time 2723.34 Seconds (without alignments) (9899.382 Million coil updates/sec 1141e: 05-09-763-292-1 Septence: 1.46 Sequence: 1.46 Sequence: 1.46 Seoring table: 10ENTITY_NUC Gapop 10.0, Gapext 1.0 Searched: 11951937 seqs, 5372889281 residues Total number of hits satisfying chosen parameters: 22703874 Minimum DB seq length: 00 Maximum BB seq length: 00 Maximum Match 100 Listing first 45 summaries Database: 1: em_estfun:* 1: em_estfun:* 2: em_estfun:* 3: em_estfun:* 5: em_estfun:* 5: em_estfun:* 6: em_estfun:* 6: em_estfun:* 7: em_estfu |   |

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E. Chases 1 to 1990)

E. Adachi, J. Alzawa, K. Akahira, S. Akimura, T. Aono, H. Arai, A. Arakawa, T. Carinici, P. Fukuda, S. Frunishi, T. Frunon, M. Hanagaki, T. Graino, P. F. Wada, S. F. Kimura, T. Frunon, M. Hanagaki, T. Rana, A. Hayatsu, M. Hiranco, K. Hiraka, I. Hori, F. Hanagaki, T. Konon, H. Kouda, K. Hiranco, K. Hiraka, I. Hori, F. Kojasa, T. Konon, H. Kowa, C. Salto, H. Sakio, R. Saki, C. Matsuyama, J. Kojasa, L. Konon, H. Chana, K. Hoda, M. Tawa, M. Kapa, S. Kutihara, C. Hatsuyama, J. Kojasa, D. Shibata, K. Shibata, F. Shibata, T. Tayan, H. Tagani, H. Tagani, M. Tagawa, A. Takahashi, F. Tanaka, T. Toya, T. Toya, T. Tayan, M. Tagan, M. 
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Best Local Similarity 76.0%; Pred. No. 4.6e-258;
Matches 1255; Conservative 0; Mismatches 392; Indels 5; Gaps
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| Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.  FIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.  Conome research. 10 (11), 1757-1771 (2000)  D. 1076661  E. (Abases 1 to 1825)  F. (Abases 1 to 1825)  F. He RIEN Genome Exploration Research Group Phase II Team and the FANTON Consortium.  Functional annotation of a full-length mouse CDNA collection  L. Nature 409, 68-690 (2001)  E. Adachi,J., Adzawa K., Akahira,S., Akimura,T. Anno,H., Arai,A.,  Arakawa,T., Carningi,P., Frutuda,S., Pokunishi,Y. Frunco,M.,  Hanagaki,T., Hara,A., Hayaksu,M., Hiramoko,K., Hiramoko,H., Karai,A.,  Hanagaki,K., Hara,A., Hayaksu,M., Hiramoko,H., Karai,A.,  Rojima,Y., Konno,H., Kouda,M., Koya,S., Kurhara,C., Marisuyama,T.,  Kojima,Y., Konno,H., Kouda,M., Koya,S., Kurhara,C., Marisuyama,T., | Myazaki, M. Nishi, K., Nomura, K., Numazaki, K., Ohno, M., Okazari, I., Okido, T., Oka, C., Salto, H., Salto, H., Salto, H., Salto, H., Santo, H., Tagawa, A., Takahashi, F., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Taka, T., Yasunishi, A., Yoshida, K., Yoshida, Y., Yoshi | cut her details.  cut her details.  cut her details.  cut her details.  cut y was prepared and sequenced in Mouse Genome  Genomic Scriences Center and Genome Exploration Research foroup in Riken  Genomic Sciences Center and Genome Science Laboratory in Riken  prepare mouse tissues. First strand cDNA was primed with a primer  prepare mouse tissues. First strand cDNA was primed with a primer  prepared by using treahlose thermo-activated reverse transcriptuse  strand CDNA, was prepared with the primer adapter of seguence[5]  strand CDNA, was prepared with the primer adapter of seguence[5]  cleaved with Xhoi and Stil. Cloning sites, 5' end: Stil. 3' end:  Xhoi. Host: Stolk  (Ab_Intel-Mocaling)   | // Assame_pre-liver* // Assame |
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| Oy 963 acagctaaagtccaggaagattgaacgtgtcattggcagaaaccggagccctgcatg 1022                     | 0y 1023 cacqacaggggccacatgcctacacagatgctgtggtgcagaggtccagagatacatc 1082   | RESULT  AKO06688  AKO06688  AKO06688  AKO06688  AKO06688  AKO06689  AKO0668  AKO06689  AKO06689  AKO06689  AKO06689  AKO06689  AKO0668  AKO06689  AKO06689  AKO06689  AKO06689  AKO06689  AKO0668  AKO06 |
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| polyA.site 1825<br>/note="putative"<br>SE COUNT 517 a 416 c 369 g 521 t 2 others<br>11GIN | Deery Match  Best Local Similarity 78.31; Score 966.6; DB 12; Length 1825;  Matches 1158; Conservative 0; Mismatches 321; Indels 0; Gaps 0;  Acantgasccuttigtggccttgggctctgctctcatgttgctctcctccaact 62  15 TCCATGATCCAATCATCTGGTCTGTCTCTCTGTGTTGTTGTCTTCTCTTCTCTTCT | 423 agcattgaggaccgtgttcaagaggaagccgctgtgtggaggagttgagaaaaacc 482 413 AGCATTGAGGACCCCTTTAAAAGACCTGCTTGTGTGAGAGATTAGAAAACC 494 483 aaagcttcaaccctgtgatccaactttcatcctgggctgtgctcctgaagtggatctg 542 415 AGCATTGAGGACCCCTTCAAAACAACTGCTTGTGTGTGAGAATTAGAAACC 494 483 aaagcttcaaccctgtgatccaactttcatccggaatggatctg 542 415 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII  |

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878 AAAAACGAGAATIATIOTOGAGAACIGGTCICACACACIGATCIGTIGCIGCIGG 847
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S. CAP trapper.

NOS MUSCLUS (strain:CS7BL/6J) adult male small intestine cDNA to musculus (strain:CS7BL/6J) adult male small intestine cDNA to musculus clone: 2010304M18; Relataoa: Chordata; Craniata; Vertebrata; Euteleostomi: Memmalia: Eutheria; Redentia; Sciurognathi: Muridae: Murinae; Mus. Remaryota, Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi: Memmalia: Eutheria; Redentia; Sciurognathi: Muridae; Murinae; Mus. Recapots (ull-length cDNA cloning metaph-efficiency full-length cDNA cloning metaph-efficiency full-length cDNA cloning metaph-efficiency; Shibata 7. Hayatsu,N., Sugahara 7., Shibata,K., Bigh-efficiency,Bushraction of cap-trapper-selected cDNAs to prepare full-length cDNA librates for rapper-selected cDNAs to prepare full-length cDNA librates for rapper-selected cDNAs to mem prepare full-length cDNA librates for rapper-selected cDNAs to prepare full-length cDNA librates for rapper-selected cDNAs to mem prepare full-length cDNA librates for rapper-selected cDNAs to mem prepare full-length cDNA librates for rapper-selected cDNAs to memoral research. 10 (10), 1617-1630 (2000)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidas; Horo.

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Barington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,

Barington,J.J., Sherf,B., Ramachandtan,R., Whittington,J.,

Lerner,L., Krashoc,D., WeElligott,R., Clark,S., Mays,R., Smith,E.,

Veloso,N., Heess,J., Cothren,R., Lo,R., Offenbacher,J., Danzia,J.
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| 124   16CTGAAGCACCCAGAGTCAAGCTAAAGTCAGGAAGAGATGAAGTGTGATTGGCA 183 | 1243<br>424<br>1303<br>484<br>1363<br>544<br>1423<br>604   | 1  | # 00 ·  |
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| 0y 1482 agracagatggtctggtctgtgtgtgtgtgtgtgtttttctttgtgggggg       | BG217233 BG217233 802 bp mRNA EST 21-AFF-2001 DEFINITION RETST\$6955 Athersys RAGE Library Homo sapiens CDNA, mRNA sequence. ACCESSION BG217233. G1:13743254 KETWORDS EST GOURCE FST ORGANISM Homon sapiens ORGANISM Homon sapiens CNGANISM Homon sapiens CNGANISM Homon sapiens AMMHAILS ENTHERIAL FINANCES CARACININI: HOMINIGAS Homo. REFERENCE 1 (Dasses 1 to 602) ANTHORS GAIG.5., Dahl.T., Transhor, D., Perry, R., Leneria, L., Carabor, D., McElligott, K., Ciark, S., Masker, S., Malth.E., Veloso, N., Hess, J., Cothren K., Lo, K., Offenbocher, J., Danily, J., and Dougs, N., TITLE Creation of Genome-vide Protein Expression Libraries using Random | Activation of Gene Expression  JOURNAL NAT. Blocechnol. 19 (5), 440 (2001) In press  COMPETED: Scott J. Cain  Athersys, Inc.  120 (Zaregete Ave, Cleveland, OH 44115, USA  120 (Zaregete Ave, Cleveland, OH 44115, USA  121: 18 (31 990)  Pax: 116 361 990  Pax: 216 361 990  Pax 117 sequence stop: 473.  FRATURES  I. 802  Anganism-Homon saplens*  Ab xref-xxon: 960e*  //db xref-xxon: 960e*  //db xref-xxon: 960e*  //cell_line="See 'Creation of Gene Expression Activation of Gene Expression Libraries sing Random Activation of Gene Expression Cell_line="See 'Creation of Gene Expression Libraries sing Random Activation See Sequence tags are not necessarily method vas used, these sequence tags are not necessarily | DASE COURT  Overy Match  Overy Match  Dest Local Similarity 91.1%; Pred, No. 8.3e-175;  Dest Local Similarity 91.1%; Pred, No. 8.3e-175;  Matches 728, Conservative 0; Mismatches 64; Indels 7; Gaps 1; Hill IIII III III IIII IIII IIII IIIIIIII |

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1 (bases 1 to 89)

8 Harrington, J. J. Sherf, B., Fundlett, S., Jackson, P. D., Perry, R., Cain, S., Dahl T., Thornton, M., Ranachandran, R., Whittington, J., Lener, L., Krashoc, D., Welligott, K., Clark, S., Mays, R., Saith, E., Veloso, N., Heas, J., Cohren, K., Lo, K., Offenbocher, J., Daniig, J., Veloso, N., Heas, J., Cohren, K., Lo, K., Offenbocher, J., Daniig, J., Veloso, N., Heas, J., Cohrens, M., Mar, Horession Libraries using Random Activation of Gene Expression

L. Mat. Biotechnol. 19 (5), 440 (2001) In press
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RST15130 Athersys RAGE Library Homo sapiens CDNA, mRNA sequence.
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Eukaryota; Metazoa: Chordata; Cranlata; Vertebrata; Eutelecatculi,

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B. Saulerr... Glabons.M., Pape, D., Harvey.N., Schurk.R., Ritter

B. Saulerr... Mouse Est Project 1999

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Contact: Marca Musabh-Mt! Mouse Est Project 1999

Contact: Marca Musabh-Mt! Mouse Est Project 1999

Mushington University School of Medicine

Mushington University School

Musconsortum (Info@imae.lini.gov) for further information

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Rarington, J., Sherf.B., Rundlett,S., Jackson,P.D., Perry,R., Cadis,S., Dahl.T.; Thornton, W. Ramendandran,R., Whittington,J., Lerner.L., Kashoc,D., McElligott,K., Clark.S., Mays.R., Smith.E., Veloso, N. Hess,J., Cothren,K., Lo.K., Offenbacher.J., Danzig,J. and Ducar M. Greation of Gene Expression Libraries using Random Activation of Gene Expression Librarys, Inc.

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88.5%; Pred, No. 3.8e-158;
tive 0; Mismatches 72; Indels 19; Gaps
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Harrington: Jo. 10)

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Calo.S. Dahl: Thornton: M. Ramachadra: R. Whittington.J.

Calo.S. Dahl: Weshoc.D. HoEBINGTE.K. Clark.S. Pays.R. Smith.E.

Veloso.N. Hess.J., Cothren.K., Lo.K., Offenbacher.J., Danzig.J.
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KST11766 Athersys RAGE Library Homo sapiens CDNA. mRNA sequence
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87.2%; Pred. No. 7.3e-151;
Live 0; Mismatches 97; Indels 2; Gaps
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    Iligated to a Draili adaptor [IGITGGCCTACTGG], digested and choned into distinct Draili sites of the parilist-TL3 become for constitution of site CACTGTTG, 3 site CACCATGG). Xhoi should be used to isolate the CDMA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Samio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5 and primer CTTCTGCTCTAAAAGCTGCG and 3 end primer CACCTGCACGAGACA.

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Pred. No. 1.1e-154;
0; Mismatches 208; Indels 6;
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Harrington, J., Sherf, B., Rundlett, S., Jackson, P. D., Perry, R., Cain, S., Dahl, T., Thornton, M., Ramachandran, R., Whittington, J., Lerner, L., Krashoc, D., McElligott, K., Clark, S., Hays, R., Smith, E., and Ducar, M., Hess, J., Cothren, K., Lo, K., Offenbacher, J., Danzig, J. and Ducar, M. of Genome-wide Protein Expression Libraries using Random Activation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression

Mat., Biotechnol, 19 (5), 440 (2001) in press
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BG205495 Athersys RAGE Library Homo saptens CDNA. mRNA sequence.
BG205076.1 GI:13726763
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                                                                 545 TIACAGAACTITAACTGAAATCTCTGGTTGACCCAAAGAACCTTGACACCACTCCAGAT 604
3201 Carnegie Are, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
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//db.rafe-"taxon:9506"
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High quality sequence stop: 354.
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Vnote-'See 'Creation of Genome-vide Protein Expression
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Rature Blockenhology, in press. Note that even though the
cell type Indicated is Hilloff, since a random activation
exhibited was used, these sequence tags are not necessarily
expressed in Hilloff under normal circumstances.
                                                                                                                                                                                                              Ouery Match 33.8%. Score 589.8. DB 11; Length 907; Best Local Similarity 86.9%, Pred. No. 3.8e-150; Indels 12; Gaps Matches 720; Conservative 0; Mismatches 97; Indels 12; Gaps
                                                  226
                                                  BASE COUNT
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us-09-763-292-1.rst

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Human.

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Evaluates. Herazoa; Chordata; Craniata; Vertebrata; Euteleostom1;

Evaluatota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;

WE Homes also fost of the fost of t
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AV553206 GLC Homo sapiens CDNA clone GLCD1E03 3', mRNA sequence.
AV553206.1 G1:9874220
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                                                                                             1574 catereacattteeetteeeceaagatetagtgaacatteageeteeattaaaaagtt 1633
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         125 c 151 g 192 t 5 others
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AUTHORS
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JOURNAL
COMMENT
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                                                                                                                                                Homan.

Exhanged: Retazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Pulkaryora: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Pakaryora: Metazoa: Chordata: Cataria: Busharyora: Manachala: Euteleostomi: Remania: Euteleostomi: Cataria: Dahilit: Chorton. W. Ramachaldran. R., Whiltington. J., Lernes: J., Ehrit. Shorton. W. Ramachaldran. R., Whiltington. J., Lernes: J., Coltren K., Lo. K., Offenbacher. J., Danzig. J. and Ducar. M. Ress. J. Cothren K., Lo. K., Offenbacher. J., Danzig. J. and Ducar. M. Gene Expression

Activation of Gene Expression

Contact: Scott J. Cain

3201 Carnegie Ave. Cleveland, OH 44115, USA

Tel: 216 361 9506

Fax: 216 361 9606

Fax: 216 361 9606
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          0 856 bp mRNA EST 21-APR-2001
Athersys RAGE Library Homo sapiens cDNA, mRNA sequence
                                                              186520
186520.1 GI:13708207
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481 TGATTCTTTCTATCATTATTTTTCTATCATA
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Search completed: April 19, 2002, 08:07:44 Job time: 2764 sec Page 1

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
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                                                                                                                April 19, 2002, 11:06:25; Search time 5830.82 Seconds (without alignments) 1200.021 Million cell updates/sec
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323
Cocctgaattgctacaacaa......aaattcatagtatcatttt 333
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Applicant; valdes, Ana
IIITE OF INVENTION: Single Nucleotide Polymorphisms Associated With ADME Genes
FILE REPERENCE: 62.0013-2 PC
CURRENT APPLICATION NUMBER: US/60/233,468
CURRENT FILING DATE: 2000-09-18
NUMBER OF SEQ ID WOS: 2488
SOUTHARE: PELL Program
ENGTH. 233
LENGTH.: 233
Morris, MacDonald
Polymorphisms Associated With ADME Genes
PCE: Gx-0013-1 P
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                                                                                     FILE REFERENCE: GX-0013-1 P
CURRENT APPLICATION NUMBER: US/60/226,176
CURRENT FILING DATE: 2000-08-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 759, Application US/60233468 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ring, Huijun Z.
Malsen, Gareth
Townley, David
Merris, MacDonald
Valdes, Ana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE: MAME/KEY: misc_feature: OTHER INFORMATION: GB:HUM2C9X05
US-60-233-468-759
                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
CTHER INFORMATION: GB:HUM2C9X05
US-60-226-176-759
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
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US-60-233-468-759
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                              Sequence 17
Sequence 77
Sequence 77
Sequence 75
Sequence 16
Sequence 65
Sequence 25
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Sequence 759, Application US/60226176
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
US-09-763-292-3
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TITLE OF INVENTION: NE
TILE REPERENCE: PLINE TO OURSELY ENLINE DATE:
CORRECT FILING DATE:
SOUTHARE: PELCHIN VOS:
SOUTHARE: PELCHIN VOS:
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RESULT 5

US-60-170-1355/C

US-60-170-1355/C

SEQUENCE 1355, APPLICATION US/60170373

SEGURAL HYPORATION:

APPLICAMT: BORDAZI; VIVIEN

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASP PROTIENS AND USES

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASP PROTIENS AND USES

TITLE OF INVENTION: THENDER DESCRIPTION: THENDER DESCRIPTION: THENDER DESCRIPTION: THENDER DESCRIPTION: THENDER DESCRIPTION: AND USES

CURRENT APPLICATION WUMBER: US/60/170,373

SOFTWARE PARE: POSS: 4299-12-13

KUNMER OF SED ID NOS: 4299-12-13

SED ID NO 1355

LENGTH 572

***CONTAMENT OF THE THENDER DESCRIPTION: AUGUST OF THENDER DESCRIPTION: AUGUST OF THE 
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US-60-181-428-187/c
US-60-181-428-187/c
Sequence 187. Application US/60181428
CEREBACH INFORMATION VIVIGE
TILLE OF INVENTION SOLUTED HUMAN DRIG-WETABOLIZING
TILLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN
TILLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN
TILLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN
TILLE OF INVENTION: DRIG-METABOLIZING PROTEINS, AND USES THEREOF
TILL PREPARED C. LOROQZY 105
CURRENT FILLING DATE: 2000-02-09
SOFTWARE: FREEDE OF WINDOWS VEFFION 4.0
LENGTH: 572
LENGTH: 572
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ORGANISM: Human
US-60-170-373-1355
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US-60-313-31-31-759

US-60-313-31-31-759

Sequence 759, Application US/6031371

SEQUENCE INFORMATION:

APPLICART: Ridg, Buijun Z.

APPLICART: Rowley, David

APPLICART: Townley, David

APPLICART: Townley, David

APPLICART: Townley, David

APPLICART: Townley, David

APPLICART: Cownley, David

TITLE OF INVERTION: Single Nucleotide Polymorphisms Associated With ADME Genes

TITLE OF INVERTION: Single Nucleotide Polymorphisms Associated With ADME Genes

CURRENT PILING DAVIE: 2001-08-16

SOUTHARE: PREL Program

SOOTHARE: PREL Program

SOOTHARE: PREL Program

TEMCH: 323

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121 gcatgcaagagcgacaggccctcacacagatgccygyggacagagacagagat 180
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Best Local Smilarity 100.0%; Pred. No. 7.4e-9 No. 7.4e-9 Northes 323; Conservative 0; Mismatches 0; Indels 0; Gaps
                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : NAME/KET: misc_feature
; OTHER INPORMATION: GB:HUM2C9X05
US-60-313-371-759
Matches 323; Conservative
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TITLE OF INVENTION: 1SOLATED HUMAN PHASE I DRUG-WETABOLIZING
TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN
TITLE OF INVENTION: DRUG-METABOLIZING PHASE I PROTEINS, AND USES THEREOF
FILE REFERENCE: LCAO0875
CURRENT PALICATION NUMBER: US/60/245,227
CURRENT FILING DATE: 2000-11-03
NUMBER OF SEQ ID NOS: 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 96.1%: Score 310.4; DB 57; Length 51955; Best Local Similarity 99.4%; Pred. No. 7.5e-85; Matches 322; Conservative 0; Mismatches 1; Indels 1; Gaps
216 ACTATCTCATTCCCAAGGTAAGTTGTTTCTCCTACACTGCAACTCCATTTCGAAGT
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                                                                                                   .50-245-227-9/c
Sequence 9. Application US/60245227
GENERAL III Desatley, Ellen manny
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// LOCATION: (1)...(51955)
// OTHER INFORMATION: n = A.T.C or G
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                                                                                                                                                                                                                                            Onery Match 96.1%; Score 310.4; DB 51; Length 572; Best Local Similarity 99.4%; Pred. No. 8.4-86; Indels 1; Gaps Matches 322; Conservative 0; Mismatches 1; Indels 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATE: BODAZII, VIVIEN
APPLICATE: BODAZII, VIVIEN
TITLE OF INVENTION: ISOLATED HUMAN DRUG-NETABOLIZING
TITLE OF INVENTION: BODAZII, VIVIEN
TITLE OF INVENTION: PROTEINS, NUCLECIC ACID MOLECULES ENCODING HUMAN
TITLE OF INVENTION: BODG-HETABOLIZING PROTEINS, AND USES THEREOF
FILE REPERENCE: CLORO327
CURRENT APPLICATION NUMBER: US-60/181,428
NUMBER OF SEN ID MOSS: 440
                                                                                                   Score 310.4, DB 51; Length 572; Best Local Similarity 99.44; Pred NO 8.4e-86; Indels 1; Indels 1; Histoha 32; Conservative 0; Hismatches 1; Indels 1;
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    US-50-181-428-187
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APPLICANT: Bessley, Ellen

TILLE OF INVENTION: ISOLATED HUMAN PHASE I DRUG-METABOLIZING
TILLE OF INVENTION: PROFIZINS, MOLLEIC CALD MOLECULES ENCODING HUMAN
TILLE OF INVENTION: PROFIZINS, MOLLEIC CALD MOLECULES ENCODING HUMAN
TILLE REFERENCE: CLOGOTOS
CURRENT FILMS DATE: 2000-06-23
CURRENT FILMS DATE: 2000-06-23
NUMBER OF SEO ID NOSS: 267
SEO ID NO SS: 267
ENCIPARE: FastSEO for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120
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                                                                                                                                                                                                                                                       RESULT 195-56
1S-60-213-795-56
Sequence 56. Application US/60213795
GENERAL INFORMATION:
APPLICATT: Beasley, Ellen
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LOCATION: (1)...(10097)
OTHER INFORMATION: n = A,T,C or G
US-60-213-795-56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Watch 92.7%; Score 299.4; DB 54; Length 10097; Best Local Similarity 99.1%; Pred No. 9.3e-82; Landels 2; (Marches 32; Conservative O; Mismatches 1; Indels 2; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ** APPLICANT** Beasley, Ellen TILLE OF THE STATE HONG-NETABOLIZING TILLE OF THYBRITOR: ISSOLATED HUMAN PRASE I DRUG-NETABOLIZING STILLE OF THYBRITOR: ISSOLATED HUMAN PRASE I PROTEINS. AND USES TILLE OF THYBRITOR: DRUG-NETABOLIZING PHASE I PROTEINS. AND USES CORRENT APPLICATION HUMBER: US/6/0/213.795 GURBER TILLE OF THE PRESENCE: CLORO/10 WORSEN US/6/213.795 GURBER OF SQUID NOS: 267 SOFTHAME: PASSISDO for Mindows Version 4.0 SQUID NO 55 LEWISDO.
   SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 9 LENGTH: 225532
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Db 54198 CCCCAAATTCATAGTATCATTTT 54175
                                                                                                                                                                                                                                                                                                                                                                                                                                      301 -cccaattcatagtatcatttt 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Application US/60213795
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PEATURE: HUMAN
PEATURE:
NAME/REI: misc_(eature
LOCATION: (1) ... (222532)
G-678TR INFORM/ION: n - A,T,C or G
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TIPE: DNA
ORGANISM: HUMAN
FEATURE:
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4; Gaps
88.0%; Score 284.2; DB 53; Length 3557; 97.9%; Pred. No. 3.1e-77; tive 0: Mismatches 3; Indels 4; Gaps
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TITLE OF INVENTION: ISOLATED HUMAN PHASE I DRUG-METAROLIZING
TITLE OF INVENTION: PROTEINS WICLEIC ACID MOLECULES ENCODING HUMAN
TITLE OF INVENTION: DRUG-METAROLIZING PHASE I PROTEINS, AND USES THE
FILE REFERENCE: CLOROMS IN SECOND SECO
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11ve 0; Mismatches 3; Indels 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 21, Application US/60207211 GENERAL INFORMATION:
           Query Match
Best Local Similarity 97.99
Matches 320; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 88.0
Best Local Similarity 97.9
Matches 320; Conservative
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: ORGANISM: HUMAN
US-60-207-211-21
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SEO ID NO 21
LENGTH: 355
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Best Local Similarity 99.1%; Pred. No. 93:2892;
Matches 32; Conservative 0; Mismatches 1; Indels 2: C
                                                                                                                                               ISOLATED HUMAN PHASE I DRUG-METABOLIZING
PROTEINS, NUCLEIC ACID MOLEGULES ENCODING HUM
DRUG-METABOLIZING PHASE I PROTEINS, AND USES
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FOR INV
                                                                                                                     APPLICANT Beasie, 1811en
TITLE OF INVESTION 1801ATEN HUCKELC ACID ITILE OF INVESTION 1800ATEN WICLEIC ACID ITILE OF INVESTION 1800ATENS, WICLEIC ACID ITILE OF INVESTION 1800ATENS. WICLEIC ACID ITILE OF INVESTION 1800ATENS
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                                                            57, Application US/60213795
INFORMATION:
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RGANISM: HUMAN
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: ORGANISM: HUM
US-69-207-211-20
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N: ISOLATED HUMAN PHASE I DRUG-METABOLIZING
DN: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN
DN: DRUG-HETABOLIZING PHASE I PROTEINS, AND USES THEREOF
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                                                                                                                                                                                                                                                                         1 ccctgaattgctacaacaatgtgccattttctccttttccatcagttttacttgg 60
2026 ccctgaattgctacaacaaatggccattttcctcctttccacagtttttacttgg 2085
                                                                                                                                                                                                                                                                                                            3: Indels 4; Gaps
                                                                                                                                                                                                                                      88.0%; Score 284.2; DB 53; Length 3557; 97.9%; Pred. No. 3.1e-77; Live 0; Mismatches 3; Indels 4;
                                                                                                                                                             for Windows Version 4.0
Pplication US/60207211
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Best Local Similarity 97.99
Matches 320; Conservative
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Search completed: April 19, 2002, 11:07:02 Job time: 13522 sec

us-09-763-292-3.rnpm

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Sequence Seq
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US. 08 - 238 - 8218 - 45
US. 08 - 145 - 6880 - 13
US. 08 - 145 - 6880 - 13
US. 08 - 145 - 6880 - 23
US. 08 - 145 - 6880 - 23
US. 08 - 145 - 6880 - 23
US. 08 - 238 - 8218 - 47
PCT - 10595 - 05744 - 51
PCT - 10595 - 05744 - 51
US. 08 - 238 - 8218 - 61
PCT - 10595 - 05744 - 51
US. 08 - 238 - 8218 - 61
US. 08 - 238 - 8218 - 62
US. 08 - 238 - 82
US. 08 - 238 - 238 - 238 - 238 - 238 - 238 - 238 - 238 - 238 - 238 - 238 - 238 - 238 - 238 - 238 - 238 - 238 - 238 - 238 - 238 - 238 - 238 - 238 - 238 - 238 - 238 - 238 - 238 - 238 - 238 - 238 - 238 - 238 - 238 - 238 - 238 - 238 - 238 - 238 - 238 - 238 - 238 - 238 - 2
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REGISTRATION NUMBER: 37,505
REFERENCE/TOOKET NUMBER: 15280-192-1
FELECOMUNICATION HYROMATION:
TELECOMUNICATION HYROMATION:
TELEFAX: (415) 326-2420
INFORMATION FOR SED ID NO:
SEQUENCE CHARACTERICS:
                                                                                                            238.2
223.6
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184.2
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99,6; Score 1739,6; DB 2: Length 1746; Best Local Similarity 99:8; Pred. No. 0; Aschber 1741; Conservative 0; Hismatches 4; Indels 0;
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LOCATION: 1.3

OTHER INFORMATION: /note- 'Corresponds to positions .5 to-1

G-07-HER INFORMATION: for 11a of Figure 2.
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CLASSIFICATION: 435
CLASSIFICATION: 435
CLASSIFICATION: 435
APPLICATION WHERE: US 08/201,118
FILING DATE: 25-EB-1994
CLASSIFICATION DATA:
APPLICATION WHERE: US 08/201,118
CLASSIFICATION: 415
PRIOR APLICATION DATA:
APPLICATION WHERE: US 07/864,962
FILING DATE: 09-APR-1992
APPORENT ACREAT HORDER: 15-20-19211
FILEDCOMMICATION HORDER: 15-20-19211
FILEDCOMMICATION HORDARATION:
TELEPROME: (650) 316-2400
FILEDCOMMICATION HORDARATION:
FILEDCOMMICATION HORDARATION 
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APPLICANT: GOLDSTEIN, JOYCE A.
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APPLICANT: GOLDSTEIN, JOYCE A.
APPLICANT: DE MORAIS, SOGIA MIF.
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Best Local Similarity 99.6; Score 1739, 6; DB 5; Length 1745;
Best Local Similarity 99.81; Pred No. 0;
Matches 1742; Conservative 0; Mismatches 4; Indels 0;
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92.9%; Pred. No. 0;
tive 0; Mismatches
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Best Local Similarity 92.9
Matches 1637; Conservative
                                              NAME: Liebeschue
REGISTRATION NUME
REFERENCE/DOCKET
                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
US-08-201-118-10
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13 AND EXPRESSION OF COMPLEMENTARY
19 OR MULIPLE MEMBERS OF THE HUMAN
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379 Lytton Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LIPE 94301
COMPUTER REALABLE FORM:
MEDIUM TIPE: Floppy disk
COMPUTER: INP PC compactal
OPERATING SISTEM: PC-005/A
SOFTWARE: Patentin Release
CURRET APPLICATION NOTA: SOFTWARE
APPLICAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: GOLDSTE
APPLICANT: ROWES:
ITILE OF INVENTION:
ITILE OF INVENTION:
ITILE OF INVENTION:
ITILE OF INVENTION:
STATES: TOMBER OF SEQUENCES:
CORRESPONDENCE ANDRES
ADDRESSET: 1979 Lytton
STREET: 379 Lytton
STRATE: California
KID: FORTHER OF STATE: CALLGORDIA
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: CLCNING, EXPRESSION AND DIAGNOSIS OF HUMAN : CTICCHROME P450 2C19: THE PRINCIPAL DETERMINANT OF S-1: MEPHENYIOIN WETABOLISH
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APPLICANT: GOLDSTEIN, Joyce A.
APPLICANT: ROMECES-PRARKS, MATJORIE
APPLICANT: ROMECES-PRARKS, MATJORIE
APPLICANT: BE WORALS, SOMIA M.F.
TITLE OF INVENTIONS: CLCANIA, EXPRESSION AND DIAGNOI
TITLE OF INVENTIONS: CYTOCHROWE P450 2C19; THE PRIII
TITLE OF INVENTIONS: CYTOCHROWE P450 2C19;
TITLE OF INVENTIONS: KEPHENYTOIN METABOLISM
NUMBER OF SEQUENCES:
CORRESS-PANDEME ADDRESS:
STREET: TWO EMBARCAGETO CENTER, 8th Floor
STREET: California
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIP: 94111

COMPUTER READABLE FORM:
WEDIGHY TPE: ILOPPY disk
COMPUTER: ILEN PC COMPALIALE
COMPUTER: ILEN PC COMPALIALE
COMPUTER: PC-TOSK-NE-DOS
SOFTHARE: PC-TOSK-NE-DOS
CLASSIFICATION NUMBER: US 08/201,118
CLASSIFICATION: UNBER: US 07/864,962
REGISTATION UNBER: US 07/864,962
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INFORMATION FOR SEQ ID NO:
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Best Local Similarity 92.91
Matches 1637; Conservative
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COCATION: 1..10
COTHER INFORMATION: COTHER INFORMATION: COTHER INFORMATION: ECUS-08-238-8218-10
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1146 ATTICATICCAACCAACCATATAATTICCTIGATTICTIGTGTACATGACACA 1205
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87.9%; Score 1534.6; DB 2; Length 1852; 92.9%; Pred. No. 0; 13ve 0; Mismatches 109; Indels 17; Gaps

RESULT 5 US-08-238-8218-10 ; Sequence 10, Application US/082388218

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PETULY 6
PCT-USSS-05744-10
Sequence 10. Application PC/TUSSS05744
GENERAL INFORMATION:
APPLICANT: BCMESS-SPARS, MAIJORIE
APPLICANT: BCMESS-SPARS, MAIJORIE
APPLICANT: DE MORES-SPARS, MAIJORIE
APPLICANT: DE MORES. SONIA M. F.
ITILE OF INVENTION: CTOCHNEW, EPPERSSION AND DIAGNOSIS OF HUMAN
TITLE OF INVENTION: CTOCHNEW, PASPESSION AND DIAGNOSIS OF HUMAN
TITLE OF INVENTION: CTOCHNEW, PASO C219: THE PRINCIPAL DETERMINANT
ITILE OF INVENTION: CTOCHNEW, PASO C219: THE PRINCIPAL DETERMINANT
ITILE OF INVENTION: CTOCHNEW, PASO C219: THE PRINCIPAL DETERMINANT
ITILE OF INVENTION: CTOCHNEW, PASO COWNER: ADDRESSEE: TOWNER: OF S-MEPHYNTOIN METABOLISM
COMPUTER: PASO ALC
STATE: CASISTOTIAL
COMPUTER: PARCHAIN Relase #1.0, Version #1.25
COMPUTER: PACHAIN Relase #1.0, Version #1.25
CURRENT APPLICATION MATA
FILING DATE: OF-MY-1994
PRIOR APPLICATION MATA
PROLICATION WIMBER: US 09/201,118
FILING DATE: OS-MY-1994
PRIOR APPLICATION WIMBER: US 09/201,118
FILING ONTE: 25-FEB-1994
PRIOR APPLICATION WIMBER: US 09/201,118
FILING ONTE: 25-FEB-1994
PRIOR APPLICATION WIMBER: US 09/201,118
FILING ONTE: 25-FEB-1994
PRIOR APPLICATION WIMBER: 29-684
FEBERENCE/DOCKET NUMBER: 29-684
FEBERENCE/DOCKET NUMBER: 15280-192-1-1
                                                                                                                                                                         1954 tgatgettettetgacegtcateteeseattteeetteeeesagatetagtgaacatt 1613 | 1111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 
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246 GATATGAGATGAAGAAGCCTGATTGATCTTGAAGAGAGATTTTGTGAAGAGGC 305
246 GATATGAGTGATGAAGAAGCCTGATTGATCTTGAAGAGAGATTTGTGGAAGAGGC 305
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                                                 INFORMATION FOR SEQ ID SEQUENCE CHARACTERIST LENGTH: 1852 base
TELEPHONE: (415)
TELEPHONE: (415)
                                                                                                                                                       HOLECULE TYPE:
PCT-US95-05744-10
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APPLICANT: GOLDSTEIN, JOyce A.
APLICANT: GOLDSTEIN, JOyce A.
TITLE OF INVENTION: CLONING AND EXPRESSION OF COMPLEMENTARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 7
US-08-201-118-4
Sequence 4, Application US/08201118
: Patent No. 5786191
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us-09-763-292-1.rni

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428 GGAGCATIGAGGACCGIGITCAAGAGGAAGCCCGCIGCCTIGIGGAGGAGTIGAGAAAA 487
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TITIE OF INVENTION: DNAS FOR MULTIPLE MEMBERS OF THE HUMAN CYTOCHROME PASO 20 TITLE OF INVENTION: SUBFAMILY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOMER OF SEQUENCES: 44
CORRESPONDERCE NUMBERS: 44
CORRESPONDERCE NUMBERS: 45
COUNTRY: 1379 LYCON Avenue
CITT: Palo Alto
STATE: California
COUNTRY: US
COMPUTER REALBLE FORM:
MEDIUM TFPE: Floppy disk
COMPUTER REALBLE FORM:
MEDIUM TFPE: Floppy disk
COMPUTER: 18M FC COMPATEL
COMPUTER: 19M FC COMPATER
COMPUTER
COMPUTER: 19M FC COMPATER
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COMPUTER: 19M FC COMPATER
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| ý6       | y 481 ccaagettcacctgtgatccac       | treatcetgggetgtgeteectgcaatgtgatet 5     |
| q        | 488 CCAAGGCCTCACCCTGTGA            | TICATCCTGGGCTGTGCTCCTGCAATGTGATCT 5      |
| oy.      | 541 getecattattttecagaaacgtt       | ittataaagatcacgaatttcitaacttgatgg 6      |
| q        | 548 GCTCCATTATTTTCCATAACGIT        | VITATAAAGATCAGCAATTTCTTAACTTAATGG 6      |
| o,       | 601 aaaaattqaatgaaaacatcagg        | aagcacccctggatccagatatgc                 |
| qq       | 608 AAAGTIGAATGAAACATCAAGA         | reaccascccissarccasarcrscartarr 6        |
| 2y       | y 661 ttcccactatcattgattatttccc    | gacccataacaattacttaaaaaccttgctt 7        |
| q        | 668 TITCICCIAICATIGATIAC           | CAACAATTACTTAAAAACGTIGCTT 7              |
| oy       | 721 ttatggaaagtgatatttgg           | scaccaagaatcgatggacatcaaca 7             |
| QQ       | 728 TTATGAAAAGTTATATTTTG           | ACACCAAGAATCAATGGACATGAACA               |
| 6y       | 781 acctcgggactttattgat            | aatggagaaggaaaagcaaaaccaac               |
| qo       | 788 ACCCTCAGGACTITATIGAT           | AATGGAGAAGGAAAGCACAACCAAC                |
| Oy       | 841 agtotgaattoactattgaa           | tgcagctgacttacttggagctggga 5             |
| đ        | 848 CATCTGAATTTACTATTGAA           | TGCAGTTGACTTGTTTGGAGCTGGGA               |
| oy.      | 901 cagagacaacaagcacaacc           | tatgeteteetteteetgetgaageacecagagg 3     |
| q        | 908 CAGAGACGACAAGCACAACC           | CTTCTCCTGCTGAAGCACCCAGAGG                |
| δλ       | 961 tcacagctaaagtccaggaa           | cattggcagaaaccggagcccctgca               |
| QQ       | 968 TCACAGCTAAAGTCCAGGAAGAGT       | SAACGTGTGTTGCAGAAACCGGAGCCCCTG           |
| 0y       | 1021 tgcacgacaggggccacatgcccta     | cagatgetgtggtgcacgaggtecagagataca 108    |
| dQ.      | 1028 IGCAAGACAGGACCACAIGCCCIA      | ACAGATGCTGTGTGCACGAGGTCCAGAGATACC 10     |
| 93       | 1081 tegaceteateceeaceagectgec     | catgcagtgacctgtgacgttaaattcagaaact 1     |
| qq       | 1088 IIGACCTICICCCCACCAGCCIGCC     | CATGCAGTGACCTGTGACATTAAATTCAGAAGT 1      |
| ò        | 1141 accteatteceaaggeacaaceat      | etteeteacttetgigetacatgacaaca 1200       |
| QQ       | 1148 AICTCATTCCCAAGGCACAACCAT      | TIAATITCCCTGACTTCTGTGCTACATGACAACA 120   |
| oy       | 1201 aagaatttcccaacccagagatgtt     | gacctcgtcacttctggatgaaggtggaaatt 1       |
| DP<br>QC | 1208 AAGAATTTCCCAACCAGAGATGTT      | ACCCICATCACTITCIGGATGAAGGTGGCAATT 1      |
| ολ       | 1261 ttaagaaaagtaactacttcatgcc     | tteteageagaaaggatttgtgtgggagagg 1320<br> |
| Q        | 1268 TIAAGAAAGIAAATACIICAIGCC      | TICICAGCAGGAAACGGATTTGTGTGGGGAGAG 13     |
| 9,       | 1321 gcctggcccgcatggagctgtttt      | attectgaeetteattttaeagaaetttaaeetga 1380 |
| q        | 1328 CCTGGCCGCATGGAGCTGTTTT        | ATTCCTGACCTCCATTTTACAGAACTTTAACCTGA 13   |
| 0.7      | 1381 aatetetgattgacecaaaggaeet     | tgacacaactcctgttgtcaatggatttgcttctg 1    |
| qq       | 1388 AAICTCIGGIIGACCCAAAGAACCI     | TGACACCACTCCAGTTGTCAATGGTTTTGCCTCTG 14   |
| 0.7      | 1441 tecegeeettetateagetgtgett     | cattectgtetgaagaageacagatggtetggetg 1500 |
| q        | 1448 IGCGCCCTTCIACCAGCIGICIN       | SATICCTGTCTGAAGAGGAGCAGATGGCCTGGCTG 1    |
| ç,       | 2y 1501 etcetgetgetgtecetgeagetete | titectetigtecaaatteactateg 1553          |
| qq       | 1508 CIGCIGIGCAGICCCIGCAGCICI      | TITCTCTGGGGCATTATCCATCTTCACTATCT         |

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Best Local Similarity 92.7%; Pred. No. 0;
Marches 154; Conservative 0; Mismatches 112; Indels 17;
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1554 tgatgcttcttctgaccgtcatctccacatttcccttccccaagatctagtgaacatt 1513 | 1141 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 
                                                                                       OTHER INFORMATION: /note- 'Corresponds to positions -12 to-1
OTHER INFORMATION: for 25 of Figure 2.*
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CORRESPONDENCE NORBESS:
ADDRESSEE: Two Barradero Center, 8th Floor
CITT: San Francisco
STATE: California
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER: US/08/238,821B
: 06-MAY-1994
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SSIPICATION: 435

(APPLICATION DATA:
LICATION NUMBER: US 07/864,962

PLICATION NUMBER: 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patentin Release #1.0, CATION DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/08238821B
Patent No. 5912120
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                             ATTORNET AGENT INFORMATION:
MANE: Litebeschuetz, Joe
REZISTRATION NUMBER: 37:
REZISTRATION NUMBER: 1TLECOMMUNICATION INFORMATII:
TELECOMMUNICATION INFORMATII
THE FERNINE: (650) 365-240
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COGOTER READALE FORM:
COMPTER: IBM PC COMPACT.
OFFTER: IBM PC COMPACT.
OFFTER: PC-TV-TARR:
DEFATING SISTEM:
TREEPER
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WOLECULE TIPE: CDNA
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APPLICATION NUM
PILING DATE: 04
CLASSIPICATION:
PRIOR APPLICATION:
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Best Local Similarity 92.74; Pred. No. 0;
Matches 1534; Conservative 0: Mismatches 112; Indels 17; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIOW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
NREMY APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                             5280-192-1-1
                                                                                                                                                                                      CURRENT APPLICATION INTA-
PRESENT APPLICATION WORDER: PCT/US5/05744
PLIASSITICATION PATA:
PRIOR APPLICATION WORDER: US 08/238.821
APPLICATION WORDER: US 08/238.821
PRIOR APPLICATION WORDER: US 08/201.118
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APPLICANT: DE MORIS, SOILE M.E.
TITLE OF INVENTION: CLOSHEM, EXPRESSION AND DIAGNOSIS OF HUMAN
TITLE OF INVENTION: CTTOCHROME P450 2C19: THE PRINCIPAL DETERMINANT
TITLE OF INVENTION: OF S-MEPHYNTION METABOLISM
NUMBER OF SEQUENCES: 61
                                                                               1081 tcgacctcatccccaccagcctgccccatgcagtgacctgtgacgttaaattcagaaact
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ADDRESSEE: Townsend a
STREET: 379 Lytton Av
CITT: Palo Alto
STATE: California
COUNTRY: US
LIP: 94301
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COMPUTER READABLE FORM
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US95-05744-4
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GENERAL INFORMATION:
APPLICANT: GOLDSTEIN, Joyce A.
APPLICANT: GOLDSTEIN, Joyce A.
APPLICANT: GOLDSTEIN, JOYCE A.
APPLICANT: GOLDSTEIN, JOYCE A.
TITLE OF INVENTION: CLONING AND EXPRESSION OF COMPLEMENTARY
TITLE OF INVENTION: SUBFANILY
TITLE OF INVENTION: SUBFANILY
NUMBER OF SCUUNCES: 44
CORRESPONDERS: 44
CORRESPONDERS: Townsend and Townsend Khourie and Crew
STREET: 3P 19 Lytton Avenue
STREET: 3P 19 Lytton Avenue
STREET: 3P 19 Lytton Avenue
STREET: 3P 2 LYTTON STREET
                                                           Ouery Match 82.3%; Score 1416.4; DB 1; Length 1892; Best Local Similarity 86.5%; Pred. No. 0; Matches 1525; Conservative 0; Mismatches 221; Indels 17; Gaps
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US-08-201-118-14
Sequence 14, Application US/08201118
FPLENT NO - 57861
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Liebeschuetz, Jos REGISTATION NUMBER: 37,505 REFERENCE/DOCKET NUMBER: 157 TELECOMUNICATION INFORMATION: TELEPHONE: (415) 326-2400 TELEFAX: (415) 326-2402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 1892 base pair
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| 121 ttggaaatatcctacagatagatattaaggatgtcagcaatccttaaccaatctctcca 180 158 TTGCANATATCCTNCAATAGATTAATTTTTTTTTTTTTTT | ### TITLE   | 5-8 GCTCCRTAATITCCATAAACGNTTGATATAAAGNTCAGAAATITGITAACITGATGG 537 601 aaaaattgaatgaaaacaatcagaattgaagaattgaagaatt 550 1111111   1111111111111111111111111111 |  | 938 CAGGAGACACAGAGACACAGAGAGAGAGAGAGAGAGAGA  | 1081 transcreateccaccagocycycocatgaggaccygaacttaacttcagaact 1140 1118 TTGACTRCTCCCACCAGCCAGCCAGCAGGACCTGANNTIAAATTCAGAACT 1177 1118 acctcattcccaaggacacaaccatataacttccctcacttctgtgctacatgacaaca 1200 11111   1 |

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218 AASTCATGGCCTGTGTACACTGTTTTGGCTGAAACCAAAGGGTGGTGGTGTGTG 277
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                                                                                               NAME/EXE: Region
LCALTON: 11.41
COTHER INFORMATION: /note= "Corresponds to positions -41 to-1
GTHER INFORMATION: for 2c of Figure 2."
                           280-19211005
                                                                         TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
            TORNET/AGENT INFORMATION NAME: Liebeschuetz, Joe REGISTRATION NUMBER: 37
                                      TELEPAN: (650) 126-24
INDEMATION POR END ID NO:
SEQUENCE CHARACTERISTICS:
LEMENT: 1822 base pair;
TIPE: nucleic acid;
TIPE: nucleic acid;
STAMDENIESS: single
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Pred. No. 0;
0; Mismatches 221; Indels 17; Gaps
                                                                                                                                                                                                                                                                            STREAT: 379 Lytton Avenue
CITT: Palo Alto
STATE: Californa
COMPRIE: Californa
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COMPRIE: Floppy disk
KEZIOM TIPE: Floppy disk
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COMPRIEN: Flop FC compatible
COMPRIEN: Flop FC compatible
COMPRIEN: Flop FC compatible
COMPRIEN: Patentin Release #1.0, Version #1.25
COMPRIENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05744
FILING DATE:
                                                                                                                                                                        COUNTIES OF INVESTIGNE CADRING, EXPRESSION AND DIAGNOS.

TITLE OF INVESTIGN: CYTOCHROME PASO 2019. THE PRINCT
ITILE OF INVESTIGN: OF S-WEPHINTIGIN METABOLLSM
WOMERS OF SEQUENCES.

CORRESPONDENCE ADDRESS:

OMBRESSET: TOWNS
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PROR APPLIANCY DATE: 32-PEB-1994
APPLIANCY DATE: 03-PAPR-1992
ATCHREY/ACBFT INFORMATION:
NAME: DOW, RATE B
RELISTRATION WOMBER: 29-684
REPERREX/COCKT HUMBER: 15280-192-1
TELEPROMICATION INFORMATION:
TELEPROME (15) 236-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION GATA.
APPLICATION HORBER: US 08/218,821
FILING DATE: 06-MAI-1994
APPLICATION HORBER: US 08/201,118
FILING DATE: 27-FEB-1994
FILIKG DATE: 27-FEB-1994
                                                                              Sequence 14, Application PC/TUS9505744 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 82.3%;
Best Local Similarity 86.5%;
Matches 1525; Conservative
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PCT-US95-05744-14
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1718 THCTHNINTNINNATHACTTTGATGTGCNCTANTGAGATAATATGHTTA 1777
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APPLICANT: GUELAN, Elizabeth H. J.
TITLE OF INVENTION: CYPERESSION AND PURIFICATION OF
TITLE OF INVENTION: CYTOCHROME P450
NUMBER OF SEQUENCES: 66
CORRESSIONES: 66
CORRESSIONES: 68
CORRESSIONES: 68
CORRESSIONES: 68
CORRESPONDENCE: 68
CORRESPONDENCE: 68
CORRESPONDENCE: 100
CIT: ALBAILA
CONTRI: GESTA
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CONTRIST RELABORALE FORM:
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20-80-194-981E-3
: Sequence 3, Application US/08194981E
: Patent NO. 5886157
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NAME: Elizabeth Selby
REGISTRATION NUMBER: 38,298
REFERENCE/DOCKET NUMBER: 226
LLECOMMUNICATION INFORMATION:
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541 ATMITICATAACGIIIGATATAAAGATCAGAATICITAAAG 600
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661 CTATCATIGATIACTICCCGGGACCAAACAAATACTAAAAAGTGCTTTATH 5 720
                                                                                          3; Gaps
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Score 1373.6; DB 2; Length 1591; Score 1373.6; DB 2; Length 1591; Best Local Similarity 93.44; Pred. No. 0; Matches 1446; Conservative 0; Mismatches 99; Indels 3;
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607 tgaatgaaaacatcagatgtaagcacccctggtcagtatgcaatatttccca 666
548 iGANIGANACATCAGAATTTGAGCACCCTGAATCACAATATTTTTC 607
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либЕR: US/O8/194,981E
February 10. 1994
: 435
                                                    FILM DAFE: February 10, 11 CLASSIFCATION: 45 ATORNEY/AGENT INFORMATION: NAME: ELIABORIA SELIAP REDISTRATION NUMBER: 38, 298 REFERENCE/DOCKET NUMBER: 22 TELECOMMUNICATION INFORMATION: TELEPRAX: (404) 688-0770 TELEPRAX: (404) 689-0770 TELEPRAX: (40
                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
SANI:SENSE: NO
US-08-194-981E-4
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US-08-198-4-
Sequence 4. Application US/08194981E
Sequence 4. Application US/08194981E
Sequence 4. Application:
APPLICART: GUENERICI, F. Peter
APPLICART: GUENERICI, F. Peter
APPLICART: GUENERICI, F. Peter
APPLICART: GUILAW
APPLICART: GUILAW
TITLE OF INVERTION: EXPRESSION AND PURIFICATION OF
TITLE OF INVERTION: EXPRESSION AND PURIFICATION OF
TITLE OF INVERTION: CUTOCHROME P450
WOMERR OF SEQUENCES: 68
CORRESPONDENCE ADDRESS: 68
CORRESPONDENCE ADDRESS: 68
CORRESPONDENCE ADDRESS: 8
ADDRESSER: Suite 1200, 127 Peachtree Street, NE
TITL AND ADDRESSER: SUBPLE 1200, 127 Peachtree Street, NE
TITL ADDRESSER: SUBPLE 1200, 127 Peachtree Street, NE
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us-09-763-292-1.rni

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Patentin Release #1.0, Version #1.25
CATION DATA:
                                                            APPLICATION NUMBER: US/UB/201,118
FILING DATE: 22-FEB-1994
CLASSITCATION: 435
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07-864,962
FILING DATE: 09-APR-1992
ATIONEY-AGENT INFORMATION:
NAME: Liebeschueta, Joe
REDISTATION UNMBER: 15.360-192-1
IELECHOWICATION INFORMATION:
TELEPHONE: (415) 126-2400
ITELEPHONE: (415) 126-2402
INFORMATION FOR SED ID NO: 6:
SEDCHOEC CHARACTERISTICS:
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                                               708/201,118
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: MOLECULE TYF
US-08-201-118-5
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APPLICANT: ROULDSTEIN, JOYCE A.

APPLICANT: ROULDSTEIN, JOYCE A.

APPLICANT: ROULDSTEIN, JOYCE A.

APPLICANT: ROULDSTEIN, JOYCE A.

TITLE OF INVENTION: DIAS FOR MULTIPLE MEMBERS OF THE HUMAN CYTCCHROME P450 2C.

TITLE OF INVENTION: SUBFMILY

TITLE OF INVENTION: SUBFMILY

TITLE OF INVENTION: SUBFMILY

TORRESPONDENCE: 444

ADDRESSE: ADDRESSE: TOWNSHING and TOWNSHING AROUNDSTEIN: CALIFORNIA

CONTRICT: 319 Lytton Avenue

CITT: Palo Alto

STARET: CALIFORNIA

CONTRICT: CALIFORNIA

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Sequence 6, Application US/08201118
Satent No. 5786191
GENERAL INFORMATION:
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Ouery Match 72.4%: Score 1264 6; DB 1; Length 2009; Best Local Similarity 84.4%; Pred. No. 0; Marches 1499; Conservative 0; Mismatches 254; Indels 22; Gaps
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| 99  | 661 ttcccactatcattgattatttcccgggaacccataacaaattacttaaaaaccttgct | icta | tcat | ttga | Ĭ. | at t | Č. | 66  | aad | CCC | řã | caa | att | act | taa | aaac | ctt | gctt | 720  |  |
|-----|---|------|------|------|----|------|----|-----|-----|-----|----|-----|-----|-----|-----|------|-----|------|--|--|
|     |   | =    | Ξ    | =    | =  | _    | Ξ  | _   | =   | =   | Ξ  | =   | _   | _   | _   | Ξ    | =   | =    |  |  |
| 355 | TCCCT   | STC  | TCAT | Š    | Ę  | ATC  | ŭ  | SAG | Ä   | Š   | ₹  | 2   | AAT | AGC | IGA | Æ    | Ē   | GCII | CTGCTCTCATCGATTATCTCCCAGGAAGTCATAAAAATAGCTGAAAATTTGCTT 914 |  |

| 1095 | 1095 CAGAGACAACGACCACCACTCTGAGATATGGACTCCTGCTGCTGCTGAAGTACCCAGAGG 1154 | 1154 |
|------|--|------|
| 961  | 961 tcacagctaaagtccaggaagagattgaacgtgtcattggcagaaaccggagccctgca 1020   | 1020 |
| 1155 | 1155 TCACAGCTAAAGTCCAGGAAGAGATTGAATGTGTAGTTGGCAGAAACGGGAGCCCCTGTA 1214 | 1214 |
| 1021 | 1021 tgcacgacaggggccacatgccctacacagatgctgtggtgcacgaggtccagagataca 1980 | 1980 |

| 1021 | 1021 tgcacgacaggggccacatgcctacacagatgctgtggtgcacgaggtccagagataca 108  | 108 |
|------|---|-----|
| 1215 | 1215 TGCAGGACAGGAGTCACATGCCCTACACAGATGCTGTGGTGCACGGGATCCAGAGATACA 127 | 127 |
| 1001 | 1081 tcgacctcatccccaccagcctgccccatgcagtgacctgtgacgttaaattcagaaact 114 | -   |
| 1275 | 1275 TTGACCTCCCCCACCACCACCCCCTGCAGTGACTGTGATTCAAAACT 133              | 133 |

| 1081 | 1081 tegaceteatececaceageetgeeecatgeagtgacetgtgacgttgaatteagaaact 1140  | 1140 |
|------|---|------|
| 1275 | 1275 TTGACCTCCCCACCACCACCTGCCCTGCACTGTGTGTTAAATTCAAAACT 1334            | 1334 |
| 1141 | 1141 acctcattcccaagggcacaaccatattaacttccctcacttctgtgctacatgacaaca 1200  | 1200 |
| 1335 | 1335 ACCTCATCCCCAAGGGCACGACGATAATAACATCCCTGACTTCTGTGCTGCTGCAATGACA 1394 | 1394 |

|   | 11111   DESTRUCTOR AND              | Lyclacatuacaata | 1200 |
|---|---|-----------------|------|
| _ | 1335 ACCTCATCCCCAAGGCCACGACCATAATAACATCCCTGACTTCTGTGCTGCCACAATGACA 1394 | TGCTGCACAATGACA | 1394 |
|   | 1201 aagaatttcccaacccagagatgtttgaccctcgtcacttctggatgaaggtggaaatt 1250   | atgaaggtggaaatt | 1250 |
|   | 1395 AAGAATTCCCCAACCCAGAGATGTTTGACCCTGGCCACTTTCTGGATAAGAGGGGCAACT 1454  | ATAAGAGIGGCAACI | 1454 |

| 음 | 1395 AAG | 1395 AAGAATTCCCCAACCCAGGGTTTTGACCCTGGCCACTTTCTGGATAAGAGTGGCAACT 1454   | 1454 |
|---|----------|--|------|
| å | 1261 tta | 1261 ttaagaaaagtaactacttcatgcctttctcagcaggaaaacggattgtgtgtg            | 1320 |
| 8 | 1455 TTA | 1455 TTAAGAAAGTGACTACTTCATGCCTTTCTCAGCAGGAAAAGGGATGTGTATGGGAGAGG 1514  | 1514 |
| Ġ | 1321 gcc | 1321 gootggcccgcatggagctgttttattcctgaccttcattttacagaactttaacctga 1380  | 1380 |
| g | 1515 GCC | 1515 GCCTGGCCCGCATGGAGCTGTTTTTATTCCTGACCACCATTTTGCAGAACTTTAACCTGA 1574 | 1574 |
| δ | 1381 aat | 1381 aatetetgattgacccaaaggacettgacacaaeteetgttgtcaatggatttgettetg 1440 | 1440 |

| 1381 | 1381 aatetetgattgacccaaaggacettgacacaactettgttgtcaatggattgcttctg 1440  | 1440 |
|------|--|------|
| 1575 | 1575 AATCTCAGGTFGACCCAAAGGATATGACATCCCCATTGCCAATGCATTTGGTCGTS 1534     | 1534 |
| 1441 | 1441 tecegecettetateagetgtgetteatteetgtetgaagaageacagatggtetggetg 1500 | 1500 |
| 1635 | 1635 TCCCACCTTGTACCAGCTCTGCTTCATTCCTGTCTGAAGAAGGGCAGATAGTTTGGCTG 1594  | 1594 |

| ^ | 1549 | 1549 atctgtgatgettettettgacegtcatetcacattttece-tteeeccaagatetagtg 1607 | 1601 |
|---|------|--|------|
| a | 1755 | 1755 GTGAGGGATAITITCICIGACTIGICAAICCACAICTICCCATICCCICAAGAICCAAIG 1914 | 1814 |
| ~ | 1608 | 1608 macattcagectecattaamaaagttteactgtgemaatatetegetatte 1659          | 1559 |
| ۵ | 1815 | GAGIIICTIGG  | 1874 |

| _ | 1815 AMCATCCAACC  | 1815 AMCATCCAACCICCATTAAAGAGATTICITGGGGCACTICCTAAATATGTGCTATTC 1874    | * D  |
|---|-------------------|--|------|
|   | 1660 cecatactetal | 1660 cccatactctataatagttacattgagtgccacataatgctgatacttgtctaatgttga 1719 | 1719 |
| _ | 1875 TCCATACTCTG  | 1875 TCCATACTCTGTATCACTIGTATTGACCACACACT-AIGCTAATACCTATCTACTGCTGA 1933 | 1933 |

<sup>1720</sup> gttættaacatattattattaaata 1744

## bb 1934 GTIGTCAGTATGTTATCACTAGAAA 1958

Search completed: April 19, 2002, 08:10:30 Job time: 2930 sec

| Description                      | L16878 Homo sapien<br>AL359672 Homo sapi<br>AL133513 Homo sapi | AL157835 Homo sapi<br>AL157835 Homo sapi<br>AL157835 Homo sapi<br>L16870 Homo sapien                                | AL153213 HOMO SAPI<br>AL1583836 HOMO SAPI<br>M74201 Rabbit Cyto<br>AF136833 HOMO SAPI<br>ACOR3888 PAFFIS DO         | AC078913 Mus muscu<br>AC078913 Mus muscu<br>M18357 Dat cutccht | ACO83911 Rattus no<br>E10631 Human cDNA      | E10853 cDNA encodi<br>M15331 Human liver                   | M21939 Human cytoc<br>S46963 putative CY<br>M51857 Himan cytoc | AR071579 Sequence<br>AR071576 Sequence<br>M61855 Human cytoc<br>D00173 Homo sapien    | E02279 Human liver<br>AR071581 Sequence | M21940 Human cytoc<br>M33545 Rat female | E14930 Artificial<br>E10866 cDNA encodi | E14931 Human mRNA<br>AR071575 Sequence | M61854 Human cytoc<br>L07093 Human cytoc | AR048195 Sequence<br>E10095 Synthetic m | E10865 cDNA encodi<br>M61856 Human cytoc | AR071580 Sequence          | M61853 Human cytoc<br>E10639 Human cDNA | Elusbz cuna encodi |  |   | 4                          | PRI   |                  | 4 -nydroxyıase.   |        | a; Vertebrata; Euteleostomi:<br>ini; Hominidae; Homo. | J.A., Faletto,M.B. and  | ry DNAs for multiple members<br>mily   |                  |  |
|----------------------------------|--|---|---|--|--|--|--|---|---|---|---|--|--|---|--|----------------------------|---|--------------------|--|---|----------------------------|-------|------------------|---|--------|---|---|--|------------------|--|
| Query<br>core Match Length DB ID | 99.6 743 9 98.1 143087 2 98.1 173154 2                         | 85.5 205/91 2<br>58.4 143087 2<br>46.6 156492 2<br>44.6 554 9   | 326 43.9 12154 2 ALL35313<br>326 43.9 205791 2 AL583836<br>280 37.7 711 4 RABP450II2<br>254.6 35.6 463 9 HSBCYP2C04 | 30.4 400 11<br>29.9 168457 2                                   | 29.2 513 10<br>24.0 163733 2<br>21.9 1473 22 | 21.9 1473 22 21.9 1576 9                                   | 21.9 1577 9<br>21.9 1814 9<br>21 9 1845 9                      | 21.9 1852<br>21.9 1854<br>21.9 1854<br>21.7 1826                                      | 21.7 1843 6<br>20.6 1892 6              | 20.5 1441 9<br>20.3 626 10              | 20.1 1444 6<br>20.1 1473 22             | 20.1 1669 6<br>20.1 1746 6             | 20.1 1746 9<br>20.1 2395 9               | 19.4 200<br>19.4 200                    | 18.9 1473 22<br>18.9 1995 9              | 18.9 2009 5<br>18.9 2258 6 | 18.9 2258<br>18.3 1473                  | 18.3 1473 22       | ALIGNMENTS                                 | - |                            |       | L16878<br>L16878 | CYP2C9; cytochrome P450; mephenytoin 4-nydroxylase 2 of 7 |        |   | <pre>1 (sites) Goldstein,J.A., Raucy,J.L., Blaisdell,J.A., Faletto,M.B.</pre> |  |                  |  |
| Result<br>No. S                  |  | Ω<br>4 Ν΄ Φ Γ~ (  |   |  |  |  |  |   |   |   |   |  |  |   |  |                            |   |                    |  | - | HUM2C9X02                  | LOCUS | ACCESSION        | SEGMENT   | SOURCE |   | REFERENCE   | TITLE  | JOURNAL MEDI INF | REFERENCE                              |
| GenCore version 4.5              | using sw model   | Run on: April 19, 2002, 09:24:59; Search time 4168.4 Seconds (without alignments) 2940.554 Million cell updates/sec | Title: US-09-763-292-2 Perfect score: 743 Sequence: 1 tcagaaatatttgaagcctgttagctcatgtgaagcgggg 743                  | Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0            | Searched: 1472140 seqs, 8248589755 residues  | Total number of hits satisfying chosen parameters: 2944280 | Minimum DB seq length: 0<br>Maximum DB seq length: 2000000000  | Post-processing: Minimum Match 0%<br>Maximum Match 100%<br>Listing first 45 summaries | gb_ba:                                  |   | 4: gb_om:*<br>5: gb_ov:*                |  | 8: gb_pl:*<br>9: gb_pr:*                 | 10: gb_ro:*<br>11: gb_sts:*             | 12: gb_sy:*<br>13: gb_un:*               |                            |   |                    | 20: en_Or:*<br>21: en_Ov:*<br>22: en_nat:* |   | 24: em_pl:*<br>25: em_ro:* |       |                  |   |        |   | em_htg_other  | Pred. No. is the number of results predicted by chance to have a<br>score greater than or equal to the score of the result being printed.<br>and is derived by analysis of the total score distribution. | ODIER KINGLIS    | )]];;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;; |

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Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
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Mammalia; Eutheria; Primates;
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|||||||||||||||||||||||||||||||||721 IIGITAGCTCATGTGAAGCGGGG 743
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Johnson,C.
Direct Submission
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Gene structure and upstream regulatory regions of human CYP2C9 and
CYP2C18
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Romkes,M., Faletto,M.B., Blaisdell,J.A., Raucy,J.L. and
Goldstein,J.A.
Correction: Cloning and expression of complementary cDNAs for
multiple members of the human cytochrome P450IIC subfamily
Biochemistry 32, 1390-1390 (1993)
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                       Biochem. Biophys. Res. Commun. 194 (1), 194-201 (1993)
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Pred. No. 1.1e-197;
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Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens chromosome 10 clone RPI1-208C17, *** SEQUENCING IN PROGRESS ***, 2 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (26-UUN-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jun 28, 2001 this sequence version replaced gi:14529836.
Assembly program: XGR4; version 4.5
Consensus quality: 14266 bases at least 040
Consensus quality: 142920 bases at least 030
Consensus quality: 142920 bases at least 020
Insert size: 142887; sum-of-contigs
Ouality coverage: 8.55x in 020 bases; sum-of-contigs quality
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• consists of 2 contigs. The true order of the pieces
• is not known and their order in this sequence record is
• arbitrary. Gaps between the contigs are represented as
• runs of N. but the exact sizes of the gaps are unknown.
• This record will be updated with the finished sequence
• as soon as it is available and the accession number will
• be preserved.
                                                                                                                                                      gagaaaaaccaagggtgggtgaccctactccatatcactgaccttactggactactatct
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HTG; HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP
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47106 143087; contig of 95982 bp in length.
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DD 150754 ICAGAAATATIIGAAGCCTGTGTGGCTGAATAAAAGCATACAAATACAATGAAAATATCA 150813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (03-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail andulifes: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jun 28, 2001 this sequence version replaced g1:14456168.
                                                                                                                                                                                                                                                                      Assembly program: XGAP4: version 4.5

Assembly program: XGAP4: version 4.5

Sequencing vector: plasmid: L08752; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Consensus quality: 173186 bases at least 040

Consensus quality: 173186 bases at least 030

Consensus quality: 173145 bases at least 020

Insert size: 173154: sum-of-contigs

Insert size: 116005; 33.1% error: agarose-fp

Oublity coverage: 6.48x in 020 bases; sum-of-contigs Quality

coverage: 9.80x in 020 bases; agarose-fp
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AL133513.11 G1:14575067
HTG; HTGS_PHASE2; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP
human.
                                                                                                                                                                                                                                                                                                                                                                                                                             * NOTE: This is a "working draft" sequence.

* This sequence will be replaced

* by the finished sequence as soon as it is available if the accession number will be preserved.

1. Occation/Qualifiers
                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 173154)
Brown, J.
Direct Submission
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Pred. No. 1.5e-194;
0; Mismatches 2;
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| 32272 c 33707 g 58012
                                                                                                                                                                                                                                    Web site: http://www.sanger.ac.uk
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*** SEQUENCING IN
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Pred. No. 1.5e-194;
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                                                                                                                                                                                                                                                                                                                         Euteleostomi;
                                                                                                                                                                                                                                                                                              Db 151294 GGGGAAGAGGAGCATTGAGGACCGTGTTCAAGAGGAAGCCCGCTGCCTTGTGGAGGAGTT 151353
                                            Db 150994 GTTTTCTGGAAGAGGCAITTTCCCACTGGCTGAAGAGCTAACAGAGGATTTGGTAGGTG 151053
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Direct Submission
Submitted (11-JUN-2001) Sanger Centre, Hinxton, Cambridgeshire, CBIO 15A, UK. E-mail enquiries: humquery%sanger.ac.uk Clone requests: clonerequest%sanger.ac.uk
On Jun 14, 2001 this sequence version replaced gi:14148873.
                                                                                                                                                                                                                                                                  600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Assembly program: XGAP4: version 4.5 Sequencing vector: plasmid; LO8752; 100% of reads Chemistry: Dye-terminator Big Dye: 100% of reads consensus quality: 20526 bases at least Q40 Consensus quality: 205560 bases at least Q30 consensus quality: 205560 bases at least Q30 lnsert size: 205691; sum-of-contigs Insert size: 188405; 9.1% error: agarose-fp quality coverage: 11.31x in Q20 bases: sum-of-contigs Quality coverage: 11.31x in Q20 bases: sum-of-contigs Quality.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-JUN-2001
SEQUENCING
                                                                                                                                                                                                                                                                  ggggaaqaggaqcattgaggaccqtgttcaagaggaagcccgctgccttgtggaggagtt
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HTG; HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLIOP
                               tgcatgtgcctgtttcagcatctgtcttggggatggggaggatggaaaacagagacttac
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Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Summary Statistics
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Mammalia; Eutheria; Primates;
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* NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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fragment_chain:1"
fragment_20791
fragment_assembly_fragment:01703
fragment_chain:1
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| corganism="Homo sapiens" | Ab. xref="teaxon:9606" | Chromosome="10" | Clone="RP11-466J14" | Clone="RP11-466J14" | 1. 88240
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                                                                                                                                                                                                                                                                                                                                                                     Euteleostomi;
27-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (26-JUN-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jun 28, 2011 this sequence version replaced gi:14529836.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Assembly program: XGRP4; version 4.5 sequencing vector: plasmidy Statistics Assembly program: XGRP4; version 4.5 sequencing vector: plasmid; L08752; 100% of reads Sequencing vector: plasmid; L08752; 100% of reads Consensus quality: 142666 bases at least 0.40 consensus quality: 142943 bases at least 0.30 consensus quality: 142920 bases at least 0.30 Insert size: 142987; sum-of-contigs insert size: 15404; agarose-fp Ouality coverage: 8.55x in 0.20 bases; sum-of-contigs Quality coverage: 7.82x in 0.20 bases; agarose-fp
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                                                                                                                                                                                                                                                                                                                      HIG; HIGS_PHASE1; HIGS_ACTIVEFIN: HIGS_DRAFT; HIGS_FULLIOP
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Catarrhini; Hominidae;
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PROCRESS ***, 2 unordered pieces.
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clone_end:SP6
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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1. .47005
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Mammalia; Eutheria; Primates;
1 (bases 1 to 143087)
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                                                                                                                                                         97653 GITGITAGCICATGIGAAGCAGGG 97676
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SEQUENCING IN
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HTG: HTGS_PHASE2: HTGS_ACTIVEFIN: HTGS_DRAFT: HTGS_FULLTOP
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RP11-361K9,
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les 164;
vector_side:left"
47106. 143087
/note="assembly_fragment:00967"
a 26155 c 27788 g 47797 t :
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Pred. No. 2.5e-
0; Mismatches
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PROGRESS ***, in ordered pieces.
AL157835
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Local Similarity 77.3%;
les 577; Conservative
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                   Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
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                                                                                              Direct Submission
Submitted (05-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequesf@sanger.ac.uk
On Jul 8, 2001 this sequence version replaced gi:14586042.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28; Gaps
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                                                                                                                                                                                                                                                                                                                                           Assembly program: XGR44; version 4.5 Sequencing vector: plasmid; L08752; 100% of reads Sequencing vector: plasmid; L08752; 100% of reads Consensus quality: 156104 bases at least 040 consensus quality: 156214 bases at least 040 consensus quality: 156214 bases at least 030 consensus quality: 15624 bases at least 030 lnsert size: 156492; sum-of-contigs lnsert size: 156975; 13.7% error; agarose-fp quality coverage: 8.34x in 020 bases; sum-of-contigs Quality coverage: 9.69x in 020 bases; sum-of-contigs Quality
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* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

Location/Qualifiers
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46.6%; Score 346.4; DB 2;
Best Local Similarity 78.1%; Pred. No. 9.7e-87;
Matches 478; Conservative 0; Mismatches 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="RPCI-11.2"
1. .156492
/note="assembly_fragment:03685
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30007 c 31050 g 52364
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Web site: http://www.sanger.ac.uk
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/db_xref="taxon:9606"
Homo sapiens
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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                                                         1 (bases 1 to 156492)
Blakey, S.
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(bases 1 to 654) de Morais, S.M., Schweikl, H., Blaisdell, J. and Goldstein, J.A. Gene structure and upstream regulatory regions of human CYP2C9 and
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                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi:
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
DD 103986 ACIGGGCAGIGGCIAIAGGGAIGGGGAGGAIGGAAAAC--AGGCIIGAAGAGGCICCIGGG 104043
                                                   Homo sapiens (library: EMBL3 library from J. A. Goldstein) liver
                                                                                                                                                                                                                                                                                                                                                                                                                  HUMZC18X02 654 bp DNA PRI 24-AUG-1993
HOmo sapiens cytochrome P4502C18 (CYP2C18) gene, exons 2 and 3.
L16870 GI: 215000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -Meorrection: Cloning and expression of complementary CDNAs for multiple members of the human cytochrome P4501IC subfamily Biochemistry 32, 1390-1390 (1993)
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3,<1. .51)</pre>
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Goldstein,J.A., Raucy,J.L., Blaisdell,J.A., Faletto,M.B.
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Romkes, Faletto, M.B., Blaisdell, J.A., Raucy, J.L. and
Goldstein, J.A.
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93326116
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/db xref="taxon:9606"
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order(L16869.1:1438. .>1668,<1.
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52. .214
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/citation=[1]
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us-09-763-292-2.rge

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requests: clonerequest@sanger.ac.uk
On Jun 28, 2001 this sequence version replaced gi:14456168
------- Genome Center
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Best Local Similarity 72.9%;
Matches 516; Conservative
                                   Center: Sanger Centre
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Homo.
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Direct Submission
Submitted (03-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,
CBIO 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             329 ggggatggggatggaaaacagagacttacagagctcctcgggcagagcttggccat 388
                                                                                                                                                                                                                                                                                                                                                                                                    272 AGGGATGGGGAGGAAAAC--AGGCTTGAGAGCTCCTGGGACAGACTTGACCTG 329
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*** SEQUENCING I
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HTG: HTGS_PHASE2; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP
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Catarrhini; Hominidae:
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                                                                                                                                                                  44.6%; Score 331.2; DB 9;
80.8%; Pred. No. 1.8e-82;
Live 0; Mismatches 78;
                                                                                                                         212
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407. .556
                                                                                                                /evidence=experimental
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Mammalia; Eutheria; Primates;
1 (bases 1 to 173154)
                                                                                                                        178 g
            215. .406
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                                                                  /gene="CYP2C18"
/citation=[1]
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/number=3
                                                                                                                         107 c
                                                                                                                                                                                          Matches 433; Conservative
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ctgttaggaattgtttcagcaatggaaagaaatggaaggagetccggcgtttctccctc 517
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                            Assembly program: XGAP4; version 4.5 Sequencing vector: plasmid; L08755; 100% of reads Sequencing vector: plasmid; L08755; 100% of reads Consensus quality: 172989 bases at least Q40 Consensus quality: 173136 bases at least Q30 Consensus quality: 173145 bases at least Q30 Insert size: 173154; sum-of-contigs at least Q20 losert size: 160005; 33.1% error; agarose-fp Ouality coverage: 6.48x in Q20 bases; sum-of-contigs Quality coverage: 6.48x in Q20 bases; sum-of-contigs Quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       • NOTE: This is a 'working draft' sequence.
• This sequence will be replaced
• by the finished sequence as soon as it is available and
• the accession number will be preserved.

Location/Qualifiers
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Pred. No. 5.5e-81;
0; Mismatches 180; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="lo"
/clone="RR11 400G3"
/clone="Ib="RPCI-11.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58012
                              Contact: humquery@sanger.ac.uk
Center code: SC
Web site: http://www.sanger.ac.uk
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32272 c 33707 g
                                                                     Center project name: bA400G3
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DEFINITION
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                 clone RP11-466J14, *** SEQUENCING IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (11-JUN-2001) Sanger Centre, Hinxton, Cambridgeshire.
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Assembly program: XARAP4: version 4.5
Assembly program: XARAP4: version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Sequencing vector: plasmid; L08752; 100% of reads
Consensus quality: 20528 bases at least 040
Consensus quality: 205540 bases at least 030
Consensus quality: 205560 bases at least 020
Insert size: 205691; sum-of-contigs
Insert size: 188405; 91% error; agarose-fp
Quality coverage: 11.31x in 020 bases; sum-of-contigs Quality;
coverage: 12.57x in 020 bases; agarose-fp
                                                                                                                           989
                                                                                                                           NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                         518 atgacgctgcggaattttgggatggggaagaggagcattgagg-accgtgttcaagagga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALS83836.11 GI:14455940
HTG; HTGS_PHASEI: HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP
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                                                                                                                                                                                                actgacettactggactactatettetetactgacattettggaaacattteagggggtgg
                                                                                                                                                                                                                                                                                       88241 88340: gap of 100 bp
88341 205791: contig of 117451 bp in length.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: humquery@sanger.ac.uk
------ Project Information
Center project name: bA466J14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center code: SC
Web site: http://www.sanger.ac.uk
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/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens chromosome 10 clone PROGRESS ***, 2 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 205791)
Mashreghi-Mohammadi,M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human.
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AL583836/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DD 187958 AIGACCCIGTGGAATIGTGGGGTGGTAAAGAGGAGCACTGGGGAAGCATGTTCAAGTGGA 187899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  969
                                                                                                                                                                                                                                            42 aaatacaatgaaaatatcatgctaaatcaggcttagcaaatggacaaaatagtaacttcg 101
                                                                                                                                                                                                                  Gaps
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Rabbit cytochrome P45011C4 (CYP2C4) gene, exons 2 and 3.
M74201
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                                                                                                                                                                                     Length 205791;
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                                                                                                                                      100
                                                                                                                                                                                                                    0; Mismatches 180;
                                                                                                                                                                                       Score 326; DB 2;
Pred. No. 5.5e-81;
/clone="RP11-466J14"
/clone_lib="RPC1-11.2"
1. .88240
//note="assembly_fragment:00191
fragment_chain:1"
88341. .205791
                                                                            notes assembly_fragment:01703
fragment_chain:1
clone_end:17
                                                                                                                      vector_side:right"
38262 c 40890 g 69845 t
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Best Local Similarity
Matches 516; Conserv
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                                                                                                                                      56694
                               misc_feature
                                                                      misc_feature
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Human

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Submitted (24-MAR-1999) Laboratory of Pharmacology and Chemistry, National Institute of Envrionmental Health Sciences, 111 Alexander Drive PO Box 12233, Research Triangle Park, NC 27709, USA Location/Qualifiers
                                                                                                                                                                  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 463)
Klose, T.S., Blaisdell, J.A. and Goldstein, J.A.
Gene Structure of CYP2C8 and Extrahepatic Distribution of the Hum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cccadgt--cagcttcctcttcttgcctgggatctcctcctagtttcgtttctcttc 457
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                                                                   12-APR-2000
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GAGGCCCGCTGCCTGGTGGAGGAGCTGAGAAAAACCAATGGTGG 531
                                                                                                                                                                                                                                                                J. Biochem. Mol. Toxicol. 13, 1-7 (1999)
2 (bases 1 to 463)
Close, T.S., Blaisdell, J.A. and Goldstein, J.A.
Direct Submission
                                                                     PRI
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Pred. No. 1.1e-63;
0; Mismatches 94;
                                                          HSBCYP2C04 463 bp DNA
Homo sapiens CYP2C gene, exons 2 and 3.
AF136833
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                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
1. .14
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/gene="CYP2C"
/number=3
a 99 c 1
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                                                                                                            AF136833.1 GI:6707882
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Best Local Similarity 78.4%;
Matches 355; Conservative
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                  membrane protein
                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

1 (bases 1 to 711)

2 hao, J.; Chan, G.; Govind, S.; Bell, P. and Remper, B.W.

Structure of 5' regions and expression of phenobarbital-inducible rabbit cytochrome P450IIC genes

DNA Cell Biol. 9, 37-48 (1990)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14 IGCTITCITIGIGATATIGGTITCTCTTCCCAGTICTCAGAACGCTAIGGCCCTGTGTIC 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9; Gaps
                                                      Oryctolagus cuniculus (strain New Zealand White) adult liver Oryctolagus cuniculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 711;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 280; DB 4; Length 71
Pred. No. 4.8e-68;
0; Mismatches 110; Indels
 M74201.1 GI:165583
cytochrome P450 IIC4; drug metabolism; microsomal
monooxygenase.
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                                                                                                                                                                                           Location/Qualifiers
1. 711
/organism=Oryctolagus cuniculus*
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/db_xref="taxon:9986"
/cell_type="hepatocyte"
/tissue_type="liver"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                        /evidence=experimental
378. .527
                                                                                                                                                                                                                                                                                                                                                                                                                              /evidence=experimental
145 c 206 g
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/gene="CYP2C4"
/number=3
                                                                                                                                                                                                                                                                                                                                           /gene="CYP2C4"
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77.38;
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Muzny, D. M., Adans, C., Adio-Oduola, B., Ali-Osman, F. B., Allen, C., Alsbrooks, S. L., Amaratunge, H. C., Are, J. R., Banks, T., Barbaria, J., Banton, J., Binage, K., Blankehorg, K., Bonnin, D., Bouce, J., Burket, C., Burrell, K. L., Burin, D., Bouce, J., Burket, C., Burrell, K. L., Burin, D., Bouce, J., Burket, C., Burrell, K. L., Burin, D., Bouce, J., Burket, C., Burrell, K. L., Burin, D., Carron, T. F., Cartor, D., Datom, E., Chavez, D., Chavez, D., Chavez, D., Chan, G., Cox, C. Coper, J., Chowdhry, I., Christopoulos, C., Claveland, C. D., Cox, C. Coyle, M.D., Datom, B., David, R., David, M., David, M., David, M., David, M., David, D., Edgad, D., Bartin, M., Edgad, M., Edgad, D., 
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                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Rodentia; Sciurognathi, Muridae; Murinae;
                                                                                                                                                           AC083888 147838 bp DNA HTG 01-APR-2001
Rattus norvegicus clone RP32-307N15, WORKING DRAFT SECUENCE, 21
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Contact: hgsc-help@bcm.tmc.edu
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419 CAGGTCTTCATTGCGCATCCTGGTTGTCAGCCC 451
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Direct Submission
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Rattus norvegicus
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NOIE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/dosgGenbank_draft_data.html).

NOIE: This is a 'working draft' sequence. It currently consists of 21 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                Sequencing vector: M13: L08821
Chemistry: Dye-primer Bodipy: 11% of reads
Chemistry: Dye-primer Bodipy: 11% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 13344 bases at least Q40
Consensus quality: 147276 bases at least Q30
Consensus quality: 147441 bases at least Q20
Estimated insert size: 136695; sum-of-contigs estimation
Quality coverage: Ox in Q20 bases; agarose-fp estimation
Quality coverage: A.7x in Q20 bases; sum-of-contigs estimation
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in unknown length
of 18694 bp in length
in unknown length
g of 951 bp in length
g of 9521 bp in length
g of 10015 bp in length
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gap of unknown length
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of 10987 bp in length
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Sequencing vector: Plasmid; M77789
Sequencing vector: M13; L08821
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/clone="RP32-307N15"
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HTG: HTGS_PHASE1; HTGS_DRAFT.
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Location/Oualifiers
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             Annealing:
Polymerization:
PCR Cycles:
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                                        3;
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                                                                                                                                                                                                                                                                                                      DE 110309 CCTTGCAGA----TGAGACTTAATGAGCTCTTCAGGCAGCTCAGAGCCATT------ 110355
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                                        Gaps
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           Length 147838
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Stanford University School of Medicine
Department of Genetics, M-344, Stanford, CA 94305,
                                        Indels
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              DB 2;
                                        0; Mismatches 144;
           Score 238.6; DB 2
Pred. No. 2.4e-56;
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Primer B: GGAGTTGAGAAAAACCAAGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Richard M. Myers
Stanford Human Genome Cent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human STS SHGC-11522.
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STS sequence, primer;
              32.1%;
69.9%;
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Unpublished (1995)
                           Best Local Similarity 69.9
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PCR profile:
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Eukaryota: Metazoa: Chordata: Craniata: Vertebrata; Buteleostomi:
Mammalia: Eutheria: Rodentia: Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 168457)
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2 (bases 1 to 168457)
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degrees C for 23 seconds
degrees C for 30 seconds
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94 degrees C for 15
62 degrees C for 27
72 degrees C for 30
30
Perkin Elmer 9600
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5:

TITLE JOURNAL

COMMENT

AUTHORS

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29.9%; Score 221.8; DB 2; Length 168457;
65.2%; Pred. No. 1.3e-51;
Live 0; Mismatches 197; Indels 13; Gaps
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of 1269 bp in length
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of 2012 bp in length
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g of 1951 bp in length
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g of 2746 bp in length
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of 2525 bp in length
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of 2116 bp in length
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of 2575 bp in length
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of 2444 bp in length
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of 2241 bp in length
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of 1927 bp in length
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of 2366 bp in length
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/strain="c57816/J"
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Han, J., Montgomery, K.T., Grills, G., Lee, E., Long, J., Pomerantz, R., Ioshikhes, I.P., Shim, C., Decker, J., Thomas, E., Perera, A., Goltz, J.S. and Rucherlapati, R. Direct Submission
Submitted (11-AUG-2000) Department of Molecular Genetics, Albert Binstein College of Medicine Genome Center, 1300 Morris Park Ave., On Dec 28, 2000 this sequence version replaced gi:1199063).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    * NOTE: This is a 'working draft' sequence. It currently consists of 47 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N. but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Chemistry: Dye-terminator Big Dye; 1008
-Consensus quality: 154996 at least 020
-Consensus quality: 146854 at least 030
-Consensus quality: 130916 at least 040
Estimated insert size: agarose-FP - N/A
-*Estimated insert size: 167537 - sum-of-contigs
Quality coverage: 4.3x sum-of-contigs - N/A
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bin/ws.exe/mouseDB/mouseSEQ/mouseseqtable.hts
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Gene structure of cytochrome P-450(M-1) specifically expressed male rat liver
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Rat cytochrome P-450(M-1) gene, exons 2 and
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/organism="Rattus norvegicus"
/db_xref="taxon:10116"
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/note="P450 intron A"
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                                                                                                          27;
                                                                                          DB 10; Length 513;
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                                                                                         Score 217.2; DB 10;
Pred. No. 2.4e-50;
0; Mismatches 123;
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                 'n
                                                 /note="P450 intron C 115 a 95 c 144 g About 1.7 kb after segment 1.
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ne: 7828 sec
/number=2
175. .318
/note="P450 i
                                                                                           Query Match 29.2%;
Best Local Similarity 69.9%;
Matches 348; Conservative (
                                          469. .>513
/note="P450
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                        319. .468
/number=3
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us-09-763-292-1.rnpn

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April 19, 2002, 08:08:00 ; Search time 232.27 Seconds (without alignments) 885.492 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pna/USO6_NEW_COMB.seq:*

2: /cgn2_6/ptodata/2/pna/USO6_NEW_COMB.seq:*

4: /cgn2_6/ptodata/2/pna/USO3_NEW_COMB.seq:*

5: /cgn2_6/ptodata/2/pna/USO8_NEW_COMB.seq:*

5: /cgn2_6/ptodata/2/pna/USO8_NEW_COMB.seq:*

7: /cgn2_6/ptodata/2/pna/USO8_NEW_COMB.seq:*

7: /cgn2_6/ptodata/2/pna/USO8_NEW_COMB.seq:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         78474 seqs, 58898373 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                           OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 200000000
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Perfect score:
Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Searched:
                                                                                                                                                                 Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

|        | lD Description | -2440 Sequence | -698-858 Sedneuce | 3-627 Sequence | 1 Sequence 621, | US-10-105-299-7204 Sequence 7204, Ap | US-09-559-013D-11 Sequence 11, Appl | 1 Sequence 11, A | 368 Sequence 358, | 01 Sequence | -12 Sequence | 2-8 Sequence 8, A | 3019 Sequence 18 | 3-526 Sequence 625, | Sequence 625, | -16494 Seguence 16494 | 522 Sequence 622, | 3 Sequence 7203. | 124 Sequence 124. | 36 Sequence 96, P | -6 Sequence 6, 1 | US-09-975-254-11513 Sequence 11513, | 254-21714 Sequence 2171 | 975-254-23846 Sequence | 175-254-14003 Sequence 1 | -103-313-103 Sequence 103. | 375-254-20507 Sequence 20507 |
|--------|----------------|----------------|-------------------|----------------|-----------------|--------------------------------------|-------------------------------------|------------------|-------------------|-------------|--------------|-------------------|------------------|---------------------|---------------|-----------------------|-------------------|------------------|-------------------|-------------------|------------------|-------------------------------------|-------------------------|------------------------|--------------------------|----------------------------|------------------------------|
| ļ      | : :<br>: :     | 9              | 9                 | 9              | 9               | 9                                    | 'n                                  | S                | 9                 | 9           |              | _                 | S                | 9                   | 9             | Ŋ                     | ø                 | 9                | 9                 | 9                 | -                | Ŋ                                   | r)                      | Ŋ                      | 'n                       | Ø                          | S                            |
|        | Match Length I | 526            | 591               | 465            | 1186            | 1186                                 | 1454                                | 1464             | 2026              | 13327       | 1530         | 1693              | 254              | 832                 | 1001          | 272                   | 1182              | 1182             | 583               | 602               | 1745             | 252                                 | 252                     | 248                    | 237                      | 2356                       | 266                          |
| Query  | Match          | 8.0            | 7.9               | 3.4            | 3.0             | 3.0                                  | 3.0                                 | 3.0              | 2.8               | 2.8         | 2.6          | 2.6               | 2.6              | 2.5                 | 2.5           | 2.4                   | 2.4               | 2.4              | 2.3               | 2.3               | 2.3              | 2.3                                 | 2.3                     | 2.3                    | 2.3                      | 2.3                        | 2.2                          |
| ·      | Score          | 139.6          | 137.2             | 59.2           | 51.8            | 51.8                                 | 51.6                                | 51.6             | 49                | 49          | 45.8         | 45.8              | 44.6             | 43.6                | 43.6          | 41.4                  | 41.4              | 41.4             | 41                | 41                | 41               | 40.8                                | 40.8                    | 40                     | 39.4                     | 39.4                       |                              |
| Result | 2              | -              | 7                 | 3              | 7               | 0                                    | 9<br>0                              | c 2              | <b>യ</b><br>ഗ     | ٥<br>د      | 10           | 11                | 12               | 13                  | 14            | 15                    | 16                | c 17             | 18                | c 19              | 20               | 21                                  | 22                      | 23                     | 24                       | 25                         | 26                           |

| Sequence 1, Appliageduence 13380, A Sequence 19229, A Sequence 19290, Sequence 102, Appliageduence 12520, A Sequence 110, Appliageduence 11, Appliageduence 110, Appliageduence 100, Appliageduence 100, Appliageduence 202, Appliageduence 25, Appliageduence 25, Appliageduence 3502, Ap |   | Associated Polynucleotides and Polyper.  |
|--|---|--|
| US-10-104-706-1<br>US-09-975-254-13380<br>US-09-9775-254-19229<br>US-09-975-254-19230<br>US-10-103-313-102<br>US-10-103-313-102<br>US-10-103-299-7189<br>US-10-105-299-7189<br>US-10-026-666-1<br>US-10-026-666-1<br>US-10-026-666-1<br>US-10-026-661-1<br>US-10-103-254-12971<br>PCT-USO2-06912-4<br>US-10-103-313-202<br>US-10-103-313-202<br>US-10-103-313-202<br>US-10-106-698-3502<br>US-10-106-698-3502  | ALIGNMENTS                              |  |
| 1756 6<br>253 5<br>253 5<br>253 5<br>11 286 5<br>11 267 5<br>10 7932 6<br>10 7932 6<br>10 10 10 10 10 10 10 10 10 10 10 10 10 1  |   | phication US/ON: ON: Colon and PAME: 2002-03 ATE: 2000-026 E: 1099-11-03 NUMBER: US E: 1999-11-03 NOM: B 644 In Ver. 3.0 In Ver. 3.0 (43) Colon: n equals feature (44) In ver. 3.0 In ver. |
| 33. 32. 33. 33. 33. 33. 33. 33. 33. 33.  | · • • • • • • • • • • • • • • • • • • • | Sequence 2440  Sequence 2440, Application US/10106698  GENERAL INFORMATION: APPLICANT: Ruben et al. TITLE OF INVENTION: Colon and Colon Cand THEOR APPLICATION NUMBER: US/10/106/65  CUBRENT FILING DATE: 1099-029 PRIOR FILING DATE: 1999-029 PRIOR FILING DATE: 1999-029 PRIOR FILING DATE: 1999-11-03 NUMBER OF SEQ ID NOS: 8544 SOFTWARE: Patentin Ver. 3.0 ED TO 2440 ED TO 3240 E |
| 22<br>28<br>32<br>32<br>33<br>33<br>33<br>33<br>33<br>33<br>33<br>33<br>33<br>33<br>33   |   | Sequence of the control of the contr |

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GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PJ207C1
CURRENT APPLICATION NUMBER: US/10/103,313
CURRENT FILING DAIE: 2002-03-12
NUMBER OF SEQ ID NOS: 650
Prior Application removed - See File Wrapper or Palm
SOFTWARE: FELLIN Ver. 2.0
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Pred. No. 2.6e-26;
0; Mismatches 169; Indels
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LOCATION: (132)...(132)
OTHER INFORMATION: n equals a.t.q, or c
NAME/KEY: misc_feature
LOCATION: (542)...(542)
OTHER INFORMATION: n equals a.t.g, or c
NAME/KEY: misc_feature
LCCATION: (550)...(550)
OTHER INFORMATION: n equals a.t.g, or c
NAME/KEY: misc_feature
LOCATION: (570)...(579)
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Best Local Similarity 58.51
Matches 238; Conservative
SOFTWARE: Patentin Ver. 3.0
SEQ ID NO 858
LENGTH: 591
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LOCATION: (590)..(590)
                                                                 TYPE: DNA
ORGANISM: Homo sapiens
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LENGIH: 465
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
FILE REFERENCE: PA005P1
CURRENT APPLICATION NUMBER: US/10/10/6,698
CURRENT FILING DATE: 2002-03-27
PRIOR FILING DATE: 2000-09-28
PRIOR FILING DATE: 1299-09-29
PRIOR FILING DATE: 1299-09-29
PRIOR FILING UNIMBER: US 60/157,137
PRIOR APPLICATION NUMBER: US 60/157,137
PRIOR FILING DATE: 1999-11-03
PRIOR FILING DATE: 1999-11-03
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57.5%; Pred. No. 5.9e-27;
live 0; Mismatches 176;
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                  CCATION: (401)...(401)

OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc_feature

LOCATION: (414)...(414)

OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc_feature

LOCATION: (419)...(419)

OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc_feature

LOCATION: (461)...(462)

OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc_feature

LOCATION: (488)...(488)

OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc_feature

LOCATION: (518)...(518)

OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc_feature

LOCATION: (518)...(518)

COTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc_feature

LOCATION: (518)...(518)

OTHER INFORMATION: n equals a,t,g, or US-10-106-698-2440
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Best Local Similarity 57.5
Matches 238; Conservative
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                                       Gaps
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 Length 465;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PJ20721
CURRENT APPLICATION NUMBER: US/10/103,313
CURRENT FILING DATE: 2002-03-12
NUMBER OF SEQ ID NOS: 653
FILOR APPLICATION removed - See File Wrapper or Palm
SOFTWARE: PatentIn Ver. 2.0
                                   0; Mismatches 193; Indels
Score 59.2; DB 6;
Pred. No. 2.5e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 621, Application US/10103313 GENERAL INFORMATION:
 Match 3.4%;
Local Similarity 47.6%;
 Query Match 3.4:
Best Local Similarity 47.6'
Matches 175; Conservative
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LENGTH: 1186
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APPLICANT: Onc, Toshiro
APPLICANT: Onc, Toshiro
APPLICANT: Nakayama, Eiichi
TIILE OF INVENTION: CANCER ASSOCIATED ANTIGENS AND USES
TIILE OF INVENTION: THEREFOR
FILE REFERENCE: L0461/7086
CURRENT APPLICATION NUMBER: US/09/559,013D
PRIOR APPLICATION NUMBER: US 60/168,353
PRIOR FILING DATE: 1999-12-01
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ROSen, et. al
ITILE OF INVENTION:
CURRENT APPLICATION NUMBER: US/10/105,299;
CURRENT FILING DATE: 2002-03-26
NUMBER OF SEQ ID NOS: 15197
Prior Application removed - See File Wrapper or Palm: SCTWARE: PATENTIN VET. 2.0
SEQ ID NO 7204
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3.0%; Score 51.6; DB 5;
Best Local Similarity 44.0%; Pred. No. 0.00037;
Matches 329; Conservative 0; Mismatches 404;
                                                                                                                                                                                                                                                                                                                                                                                3.0%; Score 51.8; DB 6; 55.2%; Pred. No. 0.0003; ative 0; Mismatches 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 11
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Best Local Similarity 55.2%
Matches 101; Conservative
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: ORGANISM: Mus musculus
US-09-559-013D-11
                                                                                                                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-105-299-7204
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 ttacttaaaaaaccttgcttttatggaaagtgatattttggagaaagtaaaagaacaccaa 751
                                                                                                                                           822 aaggaaaagcaaaaccaacagtctga---attcactattgaaaacttggtaatcactgca
                                                                                           684 AAGCAAAGGGATGCCAAAGACGAAGAGGGGCTCCACGAGGGGCACGTGCACATGTCGGTG
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                                                                       APPLICANT: Onc. Toshiro
APPLICANT: Nakayama, Elichi
TILLE OF INVENTION: CANCER ASSOCIATED ANTIGENS AND USES
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: L0461/7086
CURRENT APPLICATION NUMBER: US/09/559,013
CURRENT FILING DATE: 2000-04-26
PRIOR APPLICATION NUMBER: US 60/168,353
PRIOR FILING DATE: 1999-12-01
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SOFTWARE: FastSEQ for Windows Version 3.0
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: Sequence 11, Application US/09559013

: GENERAL INFORMATION:
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; ORGANISM: Mus musculus
US-09-559-013-11
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Length 1464;

Score 51.6; DB 5; Pred. No. 0.00037;

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Ouery Match Best Local Similarity

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Sequence 358, Application US/10106598
GENERAL INFORMATION:
APPLICANT Ruben et al.
TITLE OF INVENTION:
CUBRENT FILLS REPERENCE: PA005P1
CUBRENT FILLING DATE: 2000-03-27
CUBRENT FILLING DATE: 2000-03-28
PRIOR PRILCATION NUMBER: US/10/105,698
PRIOR PRILCATION NUMBER: CT/US00/26524
PRIOR PRILCATION NUMBER: US 60/157,137
PRIOR FILLING DATE: 1999-03-29
PRIOR FILLING DATE: 1999-11-03
PRIOR FILLING DATE: 1999-11-03
PRIOR FILLING DATE: 1999-11-03
PRIOR FILLING DATE: 1999-11-03
SOFTWARE: PREACH TOWN NUMBER: US 60/163,280
PRIOR FILLING DATE: 1999-11-03
SOFTWARE: PADENTION NUMBER: US 60/163,280
PRIOR FILLING DATE: 1999-11-03
SOFTWARE: PADENTION NUMBER: US 60/163,280
PRIOR FILLING DATE: 1999-11-03
SOFTWARE: PADENTION NUMBER: US 60/163,280
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Mismatches 404; Indels
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Matches 329;
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GENERAL INFORMATION:
APPLICANT: Rosen, et. al
ITILE OF INVENTION: Human Secreted Proteins
FILE REFERENCE: PS950
CURRENT APPLICATION NUMBER: US/10/105, 299
CURRENT FILING DAIE: 2002-03-26
NUMBER OF SEO ID NOS: 15197
Prior Application removed - See File Wrapper or Palm
SEO ID NO 7201
SEO ID NO 7201
LENGTH: 13327
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                                       FEATURE:

NAME/REY: misc_feature

LOCATION: (1326)..(1326)

OTHER INFORMATION: n equals a,t,g, or US-10-106-698-368
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; ORGANISM: Homo sapiens
US-10-105-299-7201
LENGTH: 2026
TYPE: DNA
ORGANISM: HOMO sapiens
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GENERAL INFORMATION:
TILLE OF INVENTION: Cytochrome P450s and Uses Thereof
FILE REFERENCE: 07678/100W03
CURRENT APPLICATION NUMBER: PCT/US02/06912
CURRENT FILING DAIE: 2002-03-08
PRIOR APPLICATION NUMBER: US 60/274,241
PRIOR APPLICATION NUMBER: US 60/275,597
PRIOR FILING DAIE: 2001-03-09
PRIOR FILING DAIE: 2001-03-09
PRIOR FILING DAIE: 2001-03-09
PRIOR FILING DAIE: 2001-03-13
SOFTWARE: FastSEQ for Windows Version 4.0
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                                           70;
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Pred. No. 0.012;
0; Mismatches 277;
Score 49; DB 6;
Pred. No. 0.0043;
0; Mismatches 70
Query Match
Best Local Similarity 56.5%:
Matches 91; Conservative C
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Best Local Similarity 44.6%;
Matches 225; Conservative
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GENERAL INFORMATION:
Sequence 18019, Application US/09975254
GENERAL INFORMATION:
APPLICANT: Byrum, Joseph R.
APPLICANT: Heck, Gregory R.
APLICANT: La Rosa, Thomas J.
TILLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TILLE: OF INVENTION: Plants
FILE REFERENCE: 38-21(15309)B
CURRENT APPLICATION NUMBER: US/09/975,254
CURRENT FILING DATE: 2001-10-12
PRIOR FILING DATE: 1999-03-05
PRIOR FILING DATE: 1999-03-05
SEQ ID NO 18019
LENGTH: 254
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254 gacttgaaccatcaactccttgccaccatgtcacaaacctatggtcctatatttttactc 313
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Pred. No. 0.012;
0; Mismatches 97; Indels 0
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SQUENCE 8, Application PC/TUSO206912

SGUENEAL INFORMATION:

TILE OF INVENTION: Cytochrome P450s and Uses Thereof;

FILE REFERENCE: 07678/100003

CURRENT FILING DATE: 2002-03-08

PRIOR APPLICATION NUMBER: US 60/274,241

PRIOR APPLICATION NUMBER: US 60/274,241

PRIOR APPLICATION NUMBER: US 60/275,597

PRIOR APPLICATION NUMBER: US 60/275,597

PRIOR APPLICATION NUMBER: US 60/275,597

SPIOR FILING DATE: 2001-03-09

NUMBER FILING DATE: 2001-03-03

SOFTWARE: FastSEQ for Windows Version 4.0

FEATURE OF SECTION NUMBER: US 60/275,597
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CORGANISM: Glycine max
OTHER INFORMATION: Clone ID: 700955037H1
US-09-975-254-18019
                                                             1359 attttacagaactttaacctgaaat 1383
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Best Local Similarity 51.7%;
Matches 104; Conservative
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Length 254;
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Sequence 626, Application US/10103313
Sequence 626, Application US/10103313
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PJ207C1
CURRENT APPLICATION NUMBER: US/10/103,313
CURRENT FILING DATE: 2002-03-12
NUMBER OF SEQ 1D NOS: 653
Prior Application removed - See File Wrapper or Palm
SOFTWARE: PatentIn Ver. 2.0
                                                      Indels
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58.6%; Pred. No. 0.033;
tive 0; Mismatches 64; Indels
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TILE OF INVENTION: Nucleic Acids, Proteins, and Antibodia
FILE REFERENCE: P12070103,313
CURRENT APPLICATION NUMBER: US/10/103,313
CURRENT FILING DATE: 2002-03-12
NUMBER OF SEQ ID NOS: 653
Prior Application removed · See File Wrapper or Palm SOFIWARE: Patentin Ver. 2.0
SEQ ID NO 625
LENGTH: 1001
TIPE: DNA
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Score 44.6; DB 5;
Pred. No. 0.011;
0; Mismatches 109;
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  Query Match
Best Local Similarity 50.2%;
Matches 110; Conservative (
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Best Local Similarity 58.6%
Matches 95; Conservative
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US-10-103-313-626
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RESULT 15
US-09-975-254-16494
; Sequence 16494, Application US/09975254
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.;
; APPLICANT: Heck, Gregory R.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Moleciles Associated With
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Moleciles Associated With
; TITLE OF INVENTION: Nucleic R. US/09/975,254
; CURRENT APPLICATION NUMBER: US/09/975,254
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US/09/263,191
; PRIOR FILING DATE: 1999-03-05
; WUMBER OF SEQ ID NOS: 31255
; SEQ ID NO 16494
; LENGTH: 272
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Best Local Similarity 51.7%; Pred. No. 0.076;
Matches 93; Conservative 0; Mismatches 87; Indels
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CRGANISM: Glycine max
CHER INFORMATION: Clone ID: 700953251H1
08-09-975-254-16494
                                                        Query Match
Best Local Similarity 58.6%
Matches 95; Conservative
; ORGANISM: Homo sapiens US-10-103-313-625
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Database

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The present invention relates to a method for determining gene structure when the genomic sequence is unknown. The method involves sequencing the gene across soon intron boundaries using evenly spaced primers or tiled primers. The tiled primers comprises nucleic acids that hybridise to the known cDNA sequence of the gene at about 100-300 base determined and the gene comprises the template. Gene structure can be determined without the need to sequence the entire gene. The method provides information necessary to determine gene structure and phenotypic expression without the need to sequence entire chromosomal copy of the gene or fragment. The methods are useful in germline sequence variation analysis. The method is also useful for determining the boundaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Determining structure of genes whose sequence is not known from cDNA, by sequencing the gene or gene across exon-intron boundaries using evenly spaced primers comprising nucleic acids that hybridize to the cDNA of gene
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between regions of nucleic acids that were separated by intervening sequence, and also for determining boundaries present in genes containing stroup 1 type intruors such as Tetrahymena TRNA, where self-splicing occurs in the presence of guanosine cofactor. The present sequence is human cytochrome P450 (CYP450) 2C19 gene related to the invention.
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                                                                                         Length 8437;
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                                                             Sequence 8437 BP; 2392 A; 1501 C; 1541 G; 2654 T; 349 other
                                                                                                               Indels
                                                                                           Score 622.6; DB 22;
Pred. No. 1.3e-183;
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biallelic markers. The sequences are related to various human genes including microsomal glutathione S-transferase II (MGSIII), malate decarboxylase enzyme (DMEI/MEI), cytochome P450, glutathione reductase/synthase (GSHR/GSHS), flavin-containing monooxygenases (FMO), gamma-glutamyltransferase 5 (GGTS), dipeptidase (DP), glucose 6-phosphate dehydrogenase (GFDM), phosphogluconate dehydrogenase (FCMI), and uridine diphosphate glucoronosyl transferases (UGTS). Each of these sequences contains a biallelic marker/polymorphism, which is represented in the sequence as a degenerate/undefined base. The genes to which the biallelic marker containing sequences are related are involved in drug metabolism. Sequences AMHS1594 - AAHS1599 represent the genomic sequence of the MGSIII gene products. PCR primers AAHS1599 and AAHS1500 are used in an example for the amplification of human genomic DNA fragments. The inext of a nucleotide at a DME- or MGSTII related biallelic marker in a biological sample. The method is used to determine the frequency in population of an allele of a DME- or MGSTII related biallelic marker and to select an individual for inclusion in a clinical trial of a drug treatment. The method is also used to detect association between allele
                                                           Human: biallelic marker; single nucleotide polymorphism: SNP; MGSIII: marcosomal glutarhione Stransferase II; malate decarboxylase enzyme: DMEI; WEI; cytochrome P450; glutarhione reductase; GSHR: GSHS; GGIS; flavin-containing monooxygenase; FMO; gamma-glutamyltransferase 5: flavin-ghpeptidase; DP; glucose 6-phosphate dehydrogenase; GSPDH: haplotype: phosphogluconate dehydrogenase; PGDH; drug metabolism: phenotype: uridine diphosphate glucoronosyl transferase; UGI2; asthma; hepatoxicity;
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                   Human CYP2C8 related DNA containing a biallelic polymorphism SEQ ID 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polynucleotides comprising sequences from malate decarboxylase enzyme-related biallelic markers used for genotyping .
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Sequence 1001 BP; 265 A; 185 C; 245 G; 305 T; 1 other:

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58.4%; Score 433.6; DB 21; Length 1001; 77.3%; Pred. No. 4.3e-125;
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Human: biallelic marker; single nucleotide polymorphism; SNP; MGSTII; microsomal glutathione Stransferase II; malate decarboxylase entzyme; DMEI; MEI; cytcohrome P450; glutathione reductase; GSHR; GGT5; flavin-containing monooxygenase; FMO; gamma-glutamyltransferase 5; flavin-gippebilase; DP; glucose 6-phosphate dehydrogenase; GSPBH; haplotype; phosphogluconate dehydrogenase; PGBH; haplotype; ridine diphosphate glucoronosyl transferase; UGT2: asthma; hepatoxicity;
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Sequences AAH51110-AAH51593 represent human DNA fragments which centain biallelic markers. The sequences are related to various human genes including microsomal glutathione S-transferase II (MGSIII), malate decarboxylase enzyme (DMEJ/MEI), cytochrome P450, glutathicne reductase/synthase (GSHR/GSHS), flavin-containing monooxygenases (FMO), gamma-glutamyltransferase 5 (GGTS), dipeptidase (DPH), quicose 5 phosphate contains a biallelic marker/DOlymorphism, which is represented in the contains a biallelic marker/DOlymorphism, which is represented in the sequence as a degenerate/undefined base. The genes to which the biallelic marker containing sequences are related are involved in drum metabolism. Sequence AAH51594 - AAH51599 represent the genomic sequence of the MGSIII gene and four alternative MGSIII conv. AAH51599 and AAH51500 are used in a nexample for the amplification of mann genomic DNA fragments. The invention includes a method of genotyphing comprising determining the identity of a nucleotide at a DME- or MGSTII related biallelic marker in population of an allele of a DME- or MGSTII related biallelic marker and to select an individual for inclusion in a clinical trial of a drug transment. The method is also used to determine the frequencing assays or allele specific amplification assays, sequencing assays or allele specific amplification assays, the method assays, sequencing assays or allele specific amplification assays. The method developing the allele specific and phanotype, and to detect association between haplotype and phenotype, and to detect association assays, sequencing assays or allele specific amplification assays. The method developing astays are the an individual suffers or is at risk of developing astaymance. The polynucleoptides are used, in hybridization assays, is at the developing astaymance.
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               24-MAR-2000; 2000WO-IB00403.
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flavin-containing monooxygenase; FMO; gamma-glutamyltransferase 5; dipeptidase; DF; glucose 6-phosphate dehydrogenase; 66PDH; haplotype; phosphogluconate dehydrogenase; PGDH; drug metabolism; phenotype; uridine diphosphate glucoronosyl transferase; UGT2; asthma; hepatoxicity;
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cc reductase/synthase (GSHR/GSHS), flavin-containing monooxyge:ases (FWO), gamma-glutamyltransferase 5 (GGT5), dipeptidase (DP), glucose 6-phosphate dehydrogenase (G6DBH), phosphaqluconate dehydrogenase (GBDH), and uridine cdiphosphate glucoronosyl transferases (UGT2). Each of these sequences contains a biallelic marker/polymorphism, which is represented in the sequences as a degenerate/undefined base. The genes to which the biallelic marker containing sequences are related are involved in drug metabolism. Sequences AAHSIS94 - AAHSIS98 represent the genomic sequence of the MGSTII gene and four alternative MGSTII cDNA sequences. AAHSIS906 are wisher on an example for the amplification of human genomic DNA fragments. The care wisher of a nucleotide at a DME- or MGSTII clated biallelic marker in a biological sample. The method is used to determine the frequency in population of an allele of a DME- or MGSTII related biallelic marker and constitution of an allele of a DME- or MGSTII related biallelic marker and constitution of an allele of a DME- or MGST-II related biallelic marker and constitution of an allele of a DME- or MGST-II related biallelic marker and constitution of an allele of a DME- or MGST-II related biallelic marker and constitution of an allele of a DME- or MGST-II related biallelic marker and constitution of an allele of a DME- or MGST-II related biallelic marker and constitution of an allele specific amplification assays. The method can be seed to a determine whether an individual suffers or is at risk of dereloping extermine as a stime or is at risk of developing hepatoxicity on treatment with zileuton 

Sequence 436 BP; 100 A; 94 C; 105 G; 124 T; 13 other;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cccactggctgaaagagctaacagaggatttggtaggtgtgcatgtgcctgttt~agcat 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     301 ctgictiggggatggggaggatggaaaacagagactidcagagciccicgggcawagcit 350
                                                                                                                                                                                                                                                                                                                                                                                           61 tggacaaaatagtaacttertttgetgttawetetrtetactiteetageteteaargt 120
                                                                               Gaps
                                                                                                                                                                                                                                     90
                                                                                                                                                          22 giggitgaataaaagcatacaaatacaatgaaaatatcatgitaaatcaggittagcaaa 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tgaagcagtgaaggaagccctgattgatcttggaggagagttttctggaagaaggatttt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tgaaghrgtgaaggaagccctgattgatcttggaagagagttttctggaagaggca*ttt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ctatggccctgtgttcactctgtattttggcctgaaacccatagtggtgctgca;ggata
                                                                               ::
55.9%; Score 415.4; DB 21; Length 4.5; 96.3%; Pred. No. 1.3e-119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                               13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP.
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ID AAD12247 standard: DNA; 734
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             agtttcgtttctcttcc 458
                                                                               Matches 421; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   420 agtttcgtttctcttcc
                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-SEP-2001
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    Ouery Match
                                             Local
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Human cytochrome P450 (CYP450) 2C19 gene PCR product #3.

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Structure when the genomic sequence is unknown. The method involves sequencing the gene across exon-intron boundaries using evenly spaced primers or tiled primers. The tiled primers comprises nucleic acids that hybridise to the known comprises the template. Gene structure can be intervals and the gene comprises the template. Gene structure can be repression without the need to sequence the entire gene. The method provides information necessary to determine gene. The method of sequence continuing the boundaries of analysis. The method is also useful in germline sequence variation sequence, and also for determining boundaries between regions of nucleic acids that were separated by intervening sequence, and also for determining boundaries present in genes containing group I type introns such as Tetrahymman rNAA, where self-splicing occurs in the presence of guanosine cofactor. The presence is a PCR product obtained from human cytochrome P450 (CYP450) 2C19 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                240
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                                                                                                                                                                                                                                                                                                                                                   Determining structure of genes whose sequence is not known from cDNA. by sequencing the gene or gene across exon-intron boundaries using evenly spaced primers comprising nucleic acids that hybridize to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
            Human; gene structure; phenotypic expression; guanosine cofactor;
germline variation analysis; exon-intron boundary; Tetrahymena rRNA;
cytochrome P450 2C19; CYP450 2C19; ds.

    tcagaaatatttgaagcctgtgtggctgaataaaagcatacaaatacaatgaaaatatca

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               acttcctagctctcaaaggtctatggcctgtgttcactctgtattttggcctgaaacc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  349 CCITTICTAGCTCTCAAAAATCTATGGCCCTGTGTTCACTCTGTATTTTGGCCTGGAACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 734;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 734 BP; 236 A; 170 C; 126 G; 199 T; 3 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 369; DB 22;
Pred. No. 5.3e-105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and 349L primer related to the invention.
                                                                                                                                                                                                                                                 (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 2; Fig 4; 81pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49.78;
                                                                                                                                                                                 17-JAN-2001; 2001WO-US01461
                                                                                                                                                                                                               2000US-0488127
                                                                                                                                                                                                                                                                                   Fitzgerald MS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 427; Conservative
                                                                                                                                                                                                                                                                                                                 WPI; 2001-465380/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                              W0200153529-A2
                                                                                 Homo sapiens.
                                                                                                                                                                                                               20-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                      of gene
                                                                                                                                                                                                                                                                                   Thomann H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              408
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us-09-763-292-2.rng

4

Gaps

9

Indels

45;

Mismatches

0;

Conservative

Matches 429:

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The present invention relates to a method for determining gene structure when the genomic sequence is unknown. The method involves sequencing the gene across exon-intron boundaries using everly spaced primers or tiled primers. The tiled primers comprises nucleic acids that hybridise to the known cDNA sequence of the gene at about 10-300 base intervals and the gene comprises the template. Gene structure can be determined without the need to sequence the entire gene. The method provides information necessary to determine gene structure and phenotypic expression without the need to sequence entire chromosomal copy of the gene or fragment. The method sare useful in germline sequence variation and ysis. The method is also useful for determining the boundaries
                                   tgcatgtgcctgtttcagcatctgtcttggggatggggaggatggaaaacagaggcttac 360
                                                                                                                                            420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Determining structure of genes whose sequence is not known from cDNA, by sequencing the gene or gene across exon-intron boundaries using evenly spaced primers comprising nucleic acids that hybridize to the
                                                                                                                                                                                                           25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; gene structure; phenotypic expression; quanosine cofactor; germline variation analysis; exon-intron boundary; Tetrahymana rRNA; cytochrome P450 2C19; CYP450 2C19; ds.
                                                                                                                                                                    111 AGAGCTTCTCGGGCAGAGCTTGGCCCATCCACATGGCTGCCCAGTGTCAGCTTCTTTT
                                                                                                                                     agagetectegggeagagettggeeeatecacatggetgeeeagtgteagettertet
                                                                                                                                                                                                                                                                Human cytochrome P450 (CYP450) 2C19 gene PCR product #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAD12245 standard; DNA; 557
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thomann H, Fitzgerald
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-465380/50.
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301
                                                                                                                                 361
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between regions of nucleic acids that were separated by intervening sequence, and also for determining boundaries present in genes containing group 1 type introns such as Tetrahymena rRNA, where self-spilcing occurs in the presence of guanosine cofactor. The present sequence is a PCR product obtained from human cytochrome P450 (CYP450) 2019 gene and 2350 primer related to the invention.

Score 366.2; DB 22; Length 5° Pred. No. 3.4e-104;

49.88;

Best Local Similarity

Query Match

Sequence 557 BP; 119 A; 107 C; 137 G; 167 T; 27 other;

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398
                                                                                                                               278
                                                                                                                                                                             518
                                                                                                                                                                                                                         578
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                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Determining structure of genes whose sequence is not known from cDNA, by sequencing the gene or gene across exon-intron boundaries using evenly spaced primers comprising nucleic acids that hybridize to the CDNA of gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human: gene structure; phenotypic expression; guanosine cofactor; germline variation analysis; exon-intron boundary; Tetrahymena rRNA; cytochrome P450 2C19; CYP450 2C19; ds.
                                                                                    219 ccctgattgatcttggaggagagttttctggaagaggcattttcccactggctgaaagag
          279 ctaacagaggatttggtaggtgtgcatgtgcctgttcagcatctgtcttggggatggg
                                                                                                                                                                           tgttaggaattgttttcagcaatggaaagaaatggaaggagatccggcgtttctccctca
                                                                                                                                                                                                240 tqttaggaatcgttttcagcaatggaaagagatggaaggagatccggcgtttctccctca
                                                                                                                                                                                                                     519 tgacgctgcggaattttgggatggggaagaggagcattgaggaccgtgttcaagaggaag
                                                                                                                                                                                                                                                                579 cccgctgccttgtggaggagttgagaaaa--ccaagggtgggtgaccctactccatatc
                                                                                                                                                                                                                                                                            The present invention relates to a method for determining gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human cytochrome P450 (CYP450) 2C19 gene PCR product #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 2; Fig 4: 81pp; English
                                                                                                                                                                                                                                                                                                                                                                                          ВР
                                                                                                                                                                                                                                                                                                                                                                                       AAD12249 standard; DNA; 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-JAN-2001; 2001WO-US01461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-JAN-2000; 2000US-0488127
                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thomann H, Fitzgerald MS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI: 2001-465380/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200153529-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-JUL-2001.
                                                                                                                                                                                                                                                                                                                                                                                                              AAD12249;
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                                                                                                                                                                           459
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Disclosure: Column 55-56; 91pp; English.

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sequencing the genomic sequence is unknown. The method involves sequencing the gene across exon-intron boundaries using evenly spaced primers or tiled primers. The tiled primers comprises nucleic acids that hybridise to the known cDNA sequence of the gene at about 100-300 base intervals and the gene comprises the template. Gene structure can be a further the need to sequence the entire gene. The method by provides information necessary to determine gene structure and phenotypic expression without the need to sequence entire chromosomal copy of the gene or fragment. The methods are useful in germline sequence variation analysis. The methods are useful in germline sequence variation between regions of nucleic acids that were separated by intervening sequence, and also for determining boundaries present in genes containing in the presence of guanosine cofactor. The present sequence is a PCR product obtained from human cytochrome P450 (CYP450) 2019 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                        and 367U primer related to the invention.
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Sequence 570 BP; 146 A; 101 C; 142 G; 178 T; 3 other;

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Gaps
            ;
26.0%; Score 193.2; DB 22; Length 570; 93.8%; Pred. No. 3.4e-50;
            Indels
                                                                                             Pred. No. 3.4e
0; Mismatches
            Conservative
   Local Similarity
es 212; Conserv
Query Match
      Best Loca
Matches
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Cytochrome P450; detergent; enzyme inhibitor; non-ionic; ionic; purification; drug oxidation; steroid; carcinogen; pesticide: human;
                                                                                                                                                                                                    Sandhu P;
                                                        Human cytochrome P450 2C10 variant DNA.
                                                                                                                                                                                                    Ζ,
                                                                                                                                                                                                    Gno
       BP.
       AAX22716 standard; DNA; 1419
                                                                                                                                                  94US-0194981.
                                                                                                                                                                                                   Gillam EMJ, Guengerich FP,
                                                                                                                                                                  94US-0194981
                                        (first entry)
                                                                                                                                                                                  (UYVA-) UNIV VANDERBILT.
                                       27-MAY-1999
                                                                                                 Homo sapiens
                                                                                                                                                  10-FEB-1994;
                                                                                                                                                                   LO-FEB-1994;
                                                                                                                 US5886157-A.
                                                                                                                                  23-MAR-1999
                       AAX22716;
AAX227
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Sakaki T;

Nakatsuka I,

Котаі К,

Kaneko H,

Hayashi K, Yabusaki Y;

WPI; 1995-116991/16. P-PSDB; AAR72361.

Purifying recombinant cytochrome P450 - by utilising movel combinations of detergents and enzyme inhibitors

WPI; 1999-228609/19.

(HAYA/) HAYASHI K. (SUMO ) SUMITOMO CHEM CO LID.

93JP-0180246. 93JP-0201120. 93JP-0208279.

21-JUL-1993;

20-JUL-1993; 30-JUL-1993;

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This invention describes a recombinant cytochrome P450 protein which is purified from a host cell culture using a combination of detergents and enzyme inhibitors. The method comprises (a) fractionating the host cells to prepare their membranes, (b) adding a non-ionic detergent to the membranes in a concentration of 0.8% to 2% (w/v) in a detergent:protein ratio of between 4:1 to 10:1, (c) adding an ionic detergent:protein ratio of between 2:1 to 4:1 (d) centrifuging the membrane-detergent protein ratio of between 2:1 to 4:1 (d) centrifuging the membrane-detergent mixture to remove insoluble materials and (e) purifying the protein through a diethylaminocethyl-beaded column, then through a carboxymethyl-beaded column, and finally through a hydroxylapatite column. The method is used to purify cytochrome P450 proteins which are responsible for catalysing the oxidation of drugs, steroids, carcinogens and pesticides. The method simplifies the purification of P450 proteins, by the use of improved expression vectors
                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                     126 cetageteteaaaggtetatggeeetgtgtteaetetgtattttggeetgaaacecatag 185
                                                                                                                                                                                                                                                                                                                                                                                                                                       Human cytochrome P450; amplification; PCR; primer; expression vector; yeast NADPH-P450 reductase; safety; fusion protein; metabolite; carcinogen; mutagen; liver metabolism; ds.
                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                      ;;
0
                                                                                                                                                                                                                                                                                                                                                       Length 1419;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    246 ciggaagaggcatttcccaciggcigaaagagctaacagaggattiggta 296
                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                      Sequence 1419 BP; 409 A; 332 C; 307 G; 371 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human cytochrome P450 molecular species 2C9 cDNA.
                                                                                                                                                                                                                                                                                                                                                    Score 163; DB 20;
Pred. No. 1.5e-40;
0; Mismatches 5;
                                                                                                                                                                                                                                                                       and novel detergent combinations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA087715 standard; cDNA; 1473 BP.
                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                       21.98;
97.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94EP-0111298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity 97.17
Matches 156; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-MAR-1995.
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(SUMO ) SUMITOMO CHEM CO LID.
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                                                                                                                                                                                                                                                                                                                                                                        126
                                                                                                                                                                                                                                                                                                                                                                                                                       186
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                                                                   The nucleotide sequence of the cDNA encoding the human cytochrome P450 vas amplified by PCR using the primers AA087735. The product was amplified by PCR using the primers AA087735. The product was closed into the yeast expression vectors pAAHSN or pAHRR to produce the vectors p2C9 for the expression of the cytochrome P450 alone or p2C9R for co-expression with the yeast NADPH*P450 reductase.

The vectors are used in a method for evaluating the safety of a chemical human cytochrome P450 molecular species 1A2 (AA087714), CC9, ZE1 (AA087716) or 3A4 (AA087717), or their auxillary species and variants or in cell extracts, and analysing the resulting metabolite to assess the safety of the chemical compound. The method is useful for determining vectors are the chemical compound. The method is useful for determining vectors are compounded or the method is useful for determining vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human cytochrome P450; amplified; PCR; polymerase chain reaction; primer;
liver; yeast; expression vector; NADPH-P450 reductase; ADH gene promoter;
evaluation; safety; fusion protein; metabolite; detoxification;
                                                                                                                                                                                                                                                                                                                                                                                                     126 cctagctctcaaaggtctatggcctgtgttcactctgtattttggcctgaaacccatag 185
                                                                                                                                                                                                                                                                                                                                                                               164 ccaatctctcaaaggtctatggccctgtgttcactctgtattttggcctgaaacccatag 223
                                                                                                                                                                                                                                                                                                                                   Gars
              Evaluation of safety of a chemical cpd. - using recombinant yeast expressing human cytochrome p450 and a yeast NADPH-P450 reductase
                                                                                                                                                                                                                                             a carcinogenic or mutagenic form through metabolism in the liver
                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                        Score 163; DB 16; Length 1473;
Pred. No. 1.5e-40;
0; Mismatches 5; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1473 BP; 413 A; 345 C; 319 G; 395 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human cytochrome P450 molecular species 209 gene.
          Evaluation of safety of a chemical cpd. - using
                                               Examples; Page 23-25; 124pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAT28381 standard; DNA; 1473 BP
                                                                                                                                                                                                                                                                                                        Ouery Match 21.9%;
Best Local Similarity 97.1%;
Matches 166; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMO ) SUMIIONO CHEM CO LID.
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93JP-0208279.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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P-PSDB; AAR93168.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              carcinogenic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUL-1994;
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30-JUL-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAT28381;
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This is the nucleotide sequence of the human cytochrome P450 molecular species 2C9 gene which encodes a protein of 490 amino acids. The gene was amplified from a human liver derived cDNA library as 2 fragments of 0.9 and 0.6 kb using primers AATS6925-8. The prod. was cloned into the cytochrome only or into the vector pARHS to generate the plasmid p2C9 for prodn. of the cytochrome only or into the vector pARHS to generate the plasmid p2C9 for prodn. of the cytochrome only or into the vector pARHS to generate the plasmid p2C9 for co-prodn. with the yeast NADPH-P450 reductase. The sequence is placed under control of the yeast NADPH-P450 reductase. The vectors are used in a method for evaluating the safety of a cpd. by reacting the test cpd. with recombinantly produced human cytochrome P450 mol. species 1A2 (AAT28380), 2C9, 2E1 (AAT28382), 3A4 (AAT28383) or their variants (AAT28380), 2C9, 2E1 (AAT28382), 3A4 (AAT28383) or eductase (either as a fused protein or as a cell extract) and analysing the resultant metabolite. The cpd. is considered "sife" if it is not detoxified or is metabolised to a carcinogenic cor "unsafe" if it is not detoxified or is metabolised to a carcinogenic cor "unsafe" if it is not detoxified or is sequence 1473 BP; 413 A: 345 C: 319 G: 396 T: 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cctageteteaaaggtetatggeeetgtgtteaetetgtattttggeetgaaaceeatag 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
Novel method for the evaluation of the safety of a cpd. - using a human cytochrome P450 and yeast NADPH reductase to determine whether the analyte cpd. is detoxified or metabolised to a carcinogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human derived cytochrome; P4502C9; commercial cDNA library; yeast; transfection; recombinant production; expression vector; mammal; immunisation; sensitisation; antibody; determination; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21.9%: Score 163; DB 17; Length 1473; 97.1%; Pred. No. 1.5e-40; i:e 0; Mismatches 5; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Page 20-22; 74pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human derived cytochrome P4502C9 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAI17404 standard; cDNA; 1473
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Best Local Similarity 97.17
Matches 166; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JP08027196-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-JUL-1994;
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is purified from a host cell culture using a combination of detergents and enzyme inhibitors. The method comprises (a) fractionating the host cells to prepare their membranes, (b) adding a non-ionic detergent to the membranes in a concentration of 0.8% to 2% (w/v) in a detergent: protein ratio of between 4:1 to 10:1, (c) adding an ionic detergent to the membranes in a concentration of 0.8% to 0.8% (w/v) in a detergent:protein ratio of between 7:1 to 4:1 (d) centrifying the membranes in through a diethylaminoethyl-beaded column, then through a carboxymethyl-beaded column, and finally through a protein through a diethylaminoethyl-beaded column, then through a carboxymethyl-beaded column, and finally through a hydroxylapatite column. The method is used to purify cytochrome P450 proteins which are responsible for catalysing the oxidation of drugs. Steroids, carcinogens and pesticides. The method simplifies the purification of P450 proteins, by the use of improved expression vectors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         126 cctagctctcaaaggtctatggccctgtgttcactctgtattttggcctgaaacccatag 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              164 ccaatctctcaaaggtctatggccctgtgttcactctgtattttggcctgaaacccatag 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New P450 fusion proteins - comprising a portion of a bacterial cytochrome P450 protein and a portion of a mammalian cytochrome P450.
This invention describes a recombinant cytochrome P450 protein which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacterial; mammalian: cytochrome P450; chimeric; fusion protein: oxidise: hydrocarbon: carbon-hydrogen bond; hydroxylating; bioremediation; environmental pollutant; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                      21.9%: Score 163; DB 20; Length 1591; larity 97.1%; Pred. No. 1.6e-40; Conservative 0; Mismatches 5; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   246 ctggaagaggcattttcccactggctgaaagagctaacagaggatttggta 296
                                                                                                                                                                                                                                                                                                                                                         Sequence 1591 BP; 443 A; 372 C; 353 G; 423 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalian cytochrome P450 protein CYP2C9 encoding DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 10-11: 51pp: English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 165; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB; AAY04127.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                            The present sequence encodes the human derived cytochrome (HDC) P45029, which was obtd. from a commercial cDNA library. Yeast were transfected with an expression vector contg. the HDC cDNA. cultured and then disrupted to give a microsomal fraction. The HDC was purified from the fraction, and used to immunise and sensitise a mammal. Blood was drawn from the mammal, and an anti-HDC antibody isolated. The antibody obtd. recognises HDC P4502C9, partic. at a serum dilution rate of 1:10000, and is substantially without cross reaction to other HDC P450 spp..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
                                                                            Antibody recognising human derived cytochrome P4502C9 - allows specific detection of cytochrome P450 species in humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                              *Match 21.9%; Score 163; DB 17; Length 1473; Local Similarity 97.1%; Pred. No. 1.5e-40; Los 166; Conservative 0; Mismatches 5; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     novel
                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1473 BP; 413 A; 345 C; 319 G; 396 I; 0 other;
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                                                                                                                                           Example 1; Pages 11-13; 13pp; Japanese.
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               WPI; 1996-136337/14.
P-PSDB; AAR81465.
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The present invention describes a fusion proteins comprising a portion of a bacterial cytochrome P450 protein and also a portion of a mammalian cytochrome P450 protein. The fusion protein can oxidise hydrocarbons or any compound having a carbon-hydrogen bond. The fusion protein can be used for hydroxylating a compound to be oxidised. It can also be used in the bioremediation of an environmental pollutant. Since the fusion protein is soluble, it can be subject to structural elucidation by X-ray crystallography for designing functional proteins. It can be readily expressed in soil bacteria to facilitate bioremediation. The present sequence encodes mammalian cytochrome P450 protein CYP2C9 from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cytochrome P450 2C19; human; liver; PCR; primer; detection: CYP2C19; stereospecific S-mephenytoin 4'-hydroxylase activity; polymorphism; ss.
                                                                                                                                                                                                                                                                             cctagctctcaaaggtctatggccctgtgttcactctgtattttggcctgaaacccatag 185
                                                                                                                                                                                                                                                                                                         174 ccaatctctcaaaggtctatggccctgtgttcactctgtattttggcctgaaacccatag 233
                                                                                                                                                                                                                                                                                                                                     21.9%: Score 163; DB 20; Length 1845; 97.1%: Pred. No. 1.7e-40; ive 0; Mismatches 5; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                              246 ctggaagaggcattttcccactggctgaaagagctaacagaggatttggta 296
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1845 BP; 507 A; 424 C; 380 G; 534 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product= Cytochrome P450 C9 clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Romkes-Sparks
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cytochrome P450 2C9 clone 65 coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= b
/^nnte= "Variable position"
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"Variable position"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAT11381 standard; cDNA; 1852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , 95WO-US05744.
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P-PSDB; AAR89865.
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The sequences given in AATI1378-81 encode allelic variants of cytochrome 7450 209. The majority of clones isolated from liver S33 coded for 2C9. Of the 50 clones encoding 2C9, only two allelic variants were found. 39 cof the 2C9 clones were identical with clone 65, and 11 were identical with clone 25. Clones 25 and 65 are identical in the 5' and encoding regions but contained 2 single base changes at positions 3' roncoding regions but contained 2 single base changes at positions 3' roncoding regions but contained 2 single base changes at positions clones 29c and 6b differ by one nuclectide in the coding region. The clones 29c and 6b differ by one nuclectide in the coding region at position 385. Clone 29c has a very long, 198 bp, 5' roncoding region and a polyadenylation signal 21 bases from the poly-A tail. Clone 6b olyadenylation signal 21 bases from the poly-A tail. Clone 6b olyadenylation signals with no poly-A tail. The differences in the 3' con-coding regions could represent alternate splicing, allelic variants of 2018 because they differ by only one base in the coding region. They are most similar to 2C9 (82% amino acid homology).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           126 cctageteteaaagetetatggeeetgtgtteaetetgtattttggeetgaaacecatag 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cytochrome P450; drug screening; S-mephenytoin 4'-hydroxylase; identification; mutagenic; carcinogenic; cytotoxic; haemoprotein; xenobiotic; environmental pollutant; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             174 ccaatctctcaaaggtctatggccctgtgttcactctgtattttggcctgaaacccatag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .;
       New isolated cytochrome P450 2C subfamily member - used for identifying drugs metabolised by S-mephenytoin 4'-hydroxylase activity and to develop other screening assays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1852;
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pred. No. 1.7e-40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human cytochrome P450 2C9 clone 65 cDNA.
                                                                              Example 2; Page 104; 169pp; English.
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97.18;
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92US-0864962.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 21.9
Best Local Similarity 97.1
Matches 166; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-FEB-1994;
09-APR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
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                                                                                                                                                         This sequence encodes a human cytochrome P450 2C9 polypeptide isolated from clone 65. This polypeptide is used in a method to screen for a drug that is metabolised by a cytochrome P450 having S-mephenytoin 4'-hydroxylase activity. The protein can also be used to identify a mutagenic, carcinogenic or cytotoxic compound. Cytochrome P450 are a large family of hemoprotein enzymes capable of metabolising xenobiotics such as drugs carcinogens and environmental pollutants as well as endoblotics such as steroids, fatty acids and prostaglandins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                    Screening for drugs metabolised by cytochrome P450 - for identifying mutagenic, carcinogenic, or cytotoxic compounds
                                                                                                                                                                                                                                                                                                                                                                         ::
                                                                                                                                                                                                                                                                                                                                        Length 1852;
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Pred. No. 1.7e-40;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                               Sequence 1852 BP; 514 A; 424 C; 380 G; 534 T; 0 other;
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                            Romkes-sparks M;
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97.18;
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Best Local Similarity 97.15
Matches 166; Conservative
(ROMK/) ROMKES-SPARKS M.
                                                      WPI; 1998-436528/37
                            Goldstein JA,
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Search completed: April 19, 2002, 08:15:28 Job time: 3228 sec

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Eukaryota: Metazoa: Chordata: Craniata: Vertebrata; Euteleostomi; Eukaryota: Metazoa: Chordata: Craniata: Vertebrata; Euteleostomi; Mammalia: Eutheria: Primates: Catarrhini: Hominidae: Homo.

I (bases 1 to 675)

Wu, T., Qian, B., Huang, Q., Huang, C., Kang, B., Gao, X., Xu, Z., Xiao, H.; Xu, X., Li, N., Peng, Y., Liu, F., Qu, J., Song, H., Cheng, Z., Zeng, L., Xu, S., Gu, W., Tu, Y., Jia, Ji, Fu, G., Ren, S., Zhong, M., Lu, G., Yang, Y., Gu, Y., Chen, Z. and Han, Z.

Homo sapiens CDMA GK- clones

Unpublished (2000)

Contact: Zeguang Han

Chinese National Human Genome Center at Shanghai

231 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai

Tel: 86-21-50801919(ex.45)
BGG17892 602645541
AV660643
BG563276 602582203
BG563317 602582203
BG569317 60258622
T53876 yb85f11.s1
AV697373 AV697373
AV697578 AV697373
AV697578 AV697578
AV651103 AV695778
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AV687011 AV687011
AV655255 AV655255
AV650504 AV650504
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                                                                                                                                                                                                                                   AV691273 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo saplens"
/doganism="taxon:9606"
/clone="GKCBJD11"
/clone_lib="GKC"
/tissue_type="hepatocellular carcinoma"
/dev_stage="Adult"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: hanzq@chgc.sh.cn
This clone is available at CHGC in Shanghai
                                                                                                                                                                                                                                                                                                                   ALIGNMENTS
                                                                                                                                                                                                         AV661559
AV661295
AV661281
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AV691272
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AV655255
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AV696436 AV697436
AV696538 AV696436
AV696613 AV696639
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                                                                                                                  1 tcagaaatatttgaagcctg......ttagctcatgtgaagcgggg 743
                                                                                                                                                                               22703874
         GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                            11351937 seqs, 5372889281 residues
                                                                                                                                                                             Total number of hits satisfying chosen parameters:
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Listing first 45 summaries
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AV697749
AV69436
AV697538
AV698645
AV698645
AV696645
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AV696645
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em_gss_vrt:*
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Database

Perfect score:

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AV688076

AV691273 AV691272 ~

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Similarity 77.68;
16; Conservative
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1. (Dases 1 to 628)

2. 'Au,X., Li,N., Peng',Y., Liu,F., Ou,J., Song,H., Cheng,Z., Zeng,L., Xu,S., Gu,W., Tu,Y., Eng,Y., Liu,F., Ou,J., Song,H., Cheng,Z., Zeng,L., Xu,S., Gu,W., Tu,Y., Eng,Y., Liu,F., Vu,G., Ren,S., Zhong,M., Lu,G., Yang,Y., Gu,Y., Chen,Z. and Han,Z.

Homo sapiens cDNA GK- clones

Unpublished (2000)

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Fax: 86-21-50801919

Fax: 86-21-508019202

Email: hanzgechgc.sh.cn

This clone is available at CHGC in Shanghai.
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Site_2:
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                                                                                                                                                                                                                                 443
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AV693304 GKC Homo sapiens cDNA clone GKCBIB04 5', av693304
                                                                                   Indels
/note="Vector: pBluescript sk(-);
                                                                                 0; Mismatches 113;
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                     δ
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                                                           Query Match 43.6%;
Best Local Similarity 78.2%;
Matches 415; Conservative 0
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AUTHORS
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JOURNAL
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi:
Mammalia; Eutheria: Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 631)

Wu,T., Qian,B., Huang,Q., Huang,C., Kang,B., Gao,X., Xu,Z., Xiao,H.,
Xu,X., Li,N., Peng,Y., Liu,F., Qu,J., Song,H., Cheng,Z., Zeng,I.,
Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G., Yang
,Y., Gu,Y., Chen,Z. and Han,Z.

Higho sapiens cDNA GK- clones
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AV695514 GKC Homo sapiens cDNA clone GKCBID04 5', mRNA sequence.
AV695514
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                                                                                            carcinoma'
                                                                                                                                                                                                                                                                                 DB 10;
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Mismatches 117;
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="GxCBIB04"
/clone=Lib="GKC"
/tissue_Lype="hepatocellular ca/dev_stage="Adult"
/lab_host="SOLR"
/note="Vector: pBluescript sk(-xhol"
                                                                                                                                                                                                                                                                               Score 322.8;
Pred. No. 4.7
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144 C
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Homo sapiens
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                         REFERENCE
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      Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
Chinese National Human Genome Center at Shanghai
201203, P. R. China
Tel: 86-21-50801912 (ex.45)
Fax: 86-21-50801922
Email: hanzgéchgc.sh.cn
This clone is available at CHGC in Shanghai.

Location/Oualifiers

//db.xef="texon-9606"
//clone="gCRDID04"
                                                                                                                                                                                                                                  5;
                                                                                                                                                            EcoRI: Site_2:
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de_stage="Adult"
lab_host="SOLR"
/note="Vector: pBluescript sk(-): Site_l:
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Pred. No. 4.7e-78;
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Best Local Similarity 77.6%;
Matches 416; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This clone is available at CHGC in Shang
Location/Qualifiers

1. 692
/ Organism="Homo sapiens"
/ db_xref="taxon:9606"
/ clone="GKCBIFI0"
/ clone="GKCBIFI0"
/ tissue_type="hepatocellular ca/dev_stage="Adult"
/ lab_host="SOLR"
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                                                                                                                Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Butheria; Butheria; Primates; Catarrhini; Hominidae: Homo.

(bases 1 to 651)

Wu,T., Olan, B., Homong,O., Huang,C., Kang,B., Gao,X., Xu,Z., Xiao,H., Xu,X., Li,N., Peng,Y., Liu,F., Qu,J., Song,H., Cheng,Z., Zeng,L., Xu,S., Gu,M., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G., Yang,Y., Gu,Y., Chen,Z., and Han,Z.

Homo sapiens cDNA GK- clones

Unpublished (2000)
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                                                                                                                                                                                                                                                             Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
151 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudos; Shanghai
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Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
                           25-SEP-2000 mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  380
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                AV697837 GKC Homo sapiens cDNA clone GKCBFCU5 5'.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="hepatocellular carcinoma"
/dev_stage="Adult"
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 321.8; DB 10;
Pred. No. 9e-78;
0; Mismatches 118;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           185
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="GKCBFC05"
/clone_lib="GKC"
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                                                                     AV697837.1 GI:10299700
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Homo sapiens
Eukaryota, Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi:
Eukaryota, Metazoa: Chordates; Catarrhini: Hominidae; Homo.

1 (bases 1 to 675)
Wu.T., Olam, B., Huang, O., Huang, C., Kang, B., Gao, X., Xu, Z., Xiao, H.,
Xu, X., Li, N., Peng, Y., Liu, F., Qu, J., Song, H., Cheng, Z., Zeng, L.,
Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Yang
Y., Gu, Y., Chen, Z. and Han, Z.
Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Eax: 86-21-50801912
Email: hansg²chgc.sh.cn
This clone is available at CHGC in Shanghai.
                                                                                                                                                                                  AV696436 675 bp mRNA EST 25-SEP-2000
AV696436 GKC Homo sapiens CDNA clone GKCBJA05 5', mRNA sequence.
AV696436
AV696436.1 GI:10298299
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558
                3; Gaps
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                                                                   614
                                                                 Length 675;
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/organism="Homo sapiens"
/db_ref="taxon:9606"
/clone="GKCBJA05"
/clone_lib="GKC"
/tissue_type="hepatocellular carcinoma"
/dev_stage="Adult"
/lab_host="SOLR"
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9e-78;
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Pred. No. 9e-78;
0; Mismatches 118;
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Best Local Similarity 77.43
Matches 415; Conservative
                                                                                                                                                                                                                                                                               human.
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Eukaryota: Metazoa: Chordata; Craniata; Vertebrata: Euteleostomi:

Bukaryota: Metazoa: Chordata; Craniata; Vertebrata: Euteleostomi:

Homosapia: Eutheria: Primates; Catarrhin!; Hominidae; Homo.

Totases 1 to 67)

Nu,T., Oian.B., Huang,O., Huang,C., Kang,B., Gao,X., Xu,Z., Xiao,H.,

Xu,X., Li,N., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,H., Cheng,Z., Zeng,L.,

Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G., Yang,Y., Gu,Y., Chen,Z. and Han,Z.

Homo sapiens CubN GK- clones

Int. Unpublished (2000)

Contact: Zeguang Han

Contact: Seguang Han

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AV697538 GKC Homo sapiens CDNA clone GKCBJB03 5', mRNA sequence.
AV697538
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/dev_stage="Adult"
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Pred. No. 9e-78;
0; Mismatches 118;
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/db_xref="taxon:9606"
/clone="GRCBJB03"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="GKC
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ilarity 77.48;
Conservative
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo:

E 1 (bases 1 to 677)

I (bases 1 to 677)

Wu,T., Olan, B., Huang, O., Huang, C., Kang, B., Gao, X., Xu, Z., Xiao, H., Xu, S., Gu, M., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Yang, Y., Cau, Y., Chen, Z. and Han, Z.

Homo sapiens cDNA GK- clones

Unpublished (2000)

Contact: Zeguang Han

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S1 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai

Tel: 86-21-50801992

Fax: 86-21-50801992
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5', mRNA sequence.
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/tissue_type="hepatocellular carcinoma"
/dev_stage="Adult"
/lab_host="SOLR"
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AV698646 GKC Homo sapiens cDNA clone GKCBJC11
AV698646 1 GI:10300617
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This clone is available at CHGC in Shanghai.
Location/Qualifiers
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Pred. No. 9e-78;
0; Mismatches 118; 1
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/db_xref="taxon:9606"
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Best Local Similarity 77.4 Matches 415: Conservative
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1 (bases 1 to 680)

2 Wu,T., Qian,B., Huang,O., Huang,C., Kang,B., Gao,X., Xu,Z., Xiao,H., Xu,X., Li,N., Peng,Y., Liu,F., Qu,J., Song,H., Chen,Z., Zeng,L., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M. Lu,G., Yang,Y., Gu,Y., Chen,Z. and Han,Z.

Homo sapiens cDNA GK- clones

Unpublished (2000)

Contact: Zequang Han

Contact: Zequang Han

Thinsee National Human Genome Center at Shanghai

351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudonz, Shanghai

201203, P. R. China

Tel: 86-21-50801929

Email: hanzg@chgc.sh.cn

This clone is available at CHGC in Shanghai.
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                            61
                                                                                                                    62 TCTATGGTCCTGTGTTCACCGTGTATTTTGGCATGAATCCCATAGTGGTGTTTCATGGAT
                                                           141 tctatggccctgtgttcactctgtattttggcctgaaacccatagtggtgctgcatggat
                                                                                                                                                                                                                                                 321 tctgtcttggggatggggaggatggaaaacagagacttacagagctcctcggggcabagct
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/tissue_type="hepatocellular carcinoma"
/dev_stage="Adult"
/lab_host="SOLR"
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/db_xref="taxon:9606"
/clone="GKCB1E09"
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AV696639
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Homo sapiens

Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 622)

Wu,T., Olan,B., Huang,O., Huang,C., Kang,B., Gao,X., Xu,Z., Xiao,H.,

Xu,X., Li,N., Peng,Y., Liu,F., Ou,J., Song,H., Cheng,Z., Zeng,L.,

Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G., Yang, Homo sapiens cDNA GK- clones

Unpublished (2000)
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Chinese National Human Genome Center at Shanghai
201203, P. P. China
1et: 86-21-50801919(ex.45)
Email: hanzg@chgc.sh.cn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AV697579 6ZC Homo sapiens cDNA clone GKCBJB12 5', mRNA sequence. AV697579 1 GI:10299442
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Location/Qualifiers
                                                                    Score 317; DB 10; 1
Pred. No. 1.9e-76;
0; Mismatches 121;
   u
   192
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 167
                                                                    42.7%;
ilarity 76.9%;
Conservative
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                                                                Ouery Match
Best Local Similarity
Matches 412; Conserv
177 a
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata: Euteleostomi:
Eukaryota: Metazoa; Chordata; Catarrhini; Hominidae; Homo.

Eukaryota: Metazoa; Chordata; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 646)

Mu,T., Ojan, B., Huang, O., Huang, C., Kang, B., Gao, X., Xu, Z., Xiao, H.,

Xu,X., Li,N., Peng,Y., Liu,F., Qu,J., Song,H., Cheng,Z., Zeng,L.,

Xu,X., Cu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G., Yang,

Y., Gu,Y., Chen,Z. and Han,Z.

Homo sapiens cDNA GR- clones

V., Gu,Y., Chon,Z. and Han Growe Center at Shanghai

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Fax: 86-21-50801919(ex.45)

Email: hanzq@chgc.sh.cn
  Contact: Zeguang Han
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201203, P. R. China
Tel: 86-21-50801922
Fax: 86-21-50801922
Fax: 86-21-50801922
Fax: 86-21-50801922
Fax: 86-21-50801922
Fax: 86-21-5080192
Fax: 86-21-5080192
Fax: 86-21-5080192
Fax: 86-21-5080192
Fax: 86-21-5080192
Fax: 86-21-5080193
Fax: 86-21-50
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                                                                                                                                                                                                                                                                                                                                                                                                                      2 others
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Pred. No. 6.5e-69;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                      212
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Eukaryota, Metazoa: Chordata; Craniata: Vertebrata; Euteleostomi;

Bukaryota; Metazoa: Chordata; Craniata: Vertebrata; Euteleostomi;

1 (bases 1 to 747)

Qian, B., Wu, T., Huang, O., Huang, C., Kang, B., Gao, X., Xu, Z., Xiao, H.,

**Xu, X., Li, N., Peng, Y., Liu, F., Qu, J., Song, H., Cheng, Z., Qu, J.,

**Zeng, L., Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu

Go, Yang, Y., Gu, Y., Chen, Z. and Han, Z.

Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                    7
                                                                                                                                                                            /note**Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AV646984 747 bp mRNA ESI 07-SEP-2000 AV646984 GLC Homo sapiens cDNA clone GLCATD11 3', mRNA sequence. AV646984
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1. .622
/organism="Homo sapiens"
/db_xref="texon:9606"
/clone="GKCBJB12"
/clone_lib="GKC"
/tissue_type="hepatocellular carcinoma"
/dev_stage="Adult"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                    Score 314.8; DB 10; Length
Pred. No. 7.5e-76;
0; Mismatches 122; Indels
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Best Local Similarity 76.7%;
Matches 411; Conservative
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1 (bases 1 to 721)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collectio:: (MGC) Unpublished (1999)
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602645541F1 NIH_MGC_76 Homo sapiens CDNA clone IMAGE:47£5890
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Pred. No. 2.5e-65:
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BG617892.1 GI:13669263
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Homo sapiens

Eukaryota, Metazoa; Chordala; Craniata; Vertebrata; Euteleostomi;

Mammalia: Eutheria: Primatesa Catarrhini; Hominidae; Homo.

Muz., Catarrhini; Hominidae; Homo.

Muz., Catarrhini; Hominidae; Homo.

Muz., Catarrhini; Homon, Homo.

Muz., Catarrhini; Homon, Homon, Homon, Homo.

Muz., Catarrhini; Homon, H
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AV695838 GKC Homo sapiens cDNA clone GKCBEE06 5', mRNA sequence.
AV695838.1 GI:10297701
Contact: Robert Strausberg, Ph.D.
Email: cgapbs r@mail.nih.gov
Tissue procurement CLONETECH Laboratories, Inc.
cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M. A.G.E. Consortium (LLNL)
DNA Sequencing by: They Genomics, Inc.
cLone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov. b column: 11
High quality: sequence stop: 718.
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                                                                                                                    1. .530
/organism="Homo sapiens"
/db_aref="taxon:9606"
/db_aref="taxon:9606"
/clone_lib="GKCBEE06"
/tissue_type="hepatocellular carcinoma"
/dev_stage="Adult"
/lab_host="SOLR"
/note="Vector: pBluescript sk(-): Site_1: EcoRI: Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AV660643 395 bp mRNA ESF 07-SEP-2000 AV660643 GLC Homo sapiens cDNA clone GLCGJG12 3', mRNA sequence. AV660643
                                              Shanghai
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                                                                                                                                                                                                                                                                                          Gaps
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Homo sapiens cDNA GK- clones
Unpublished (2000)
Contact: Zeguang Human
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Sha
701203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Email: harag@chgc.sh.cn
This clone is available at CHGC in Shanghai.
                                                                                                                                                                                                                                                                    Score 267.4; DB 10: Length 530:
Pred. No. 8e-63;
0; Mismatches 121; Indels 12;
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Best Local Similarity 74.7%;
Matches 392; Conservative (
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/dev_stage="Adult"
/lab_host="SOLR"
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                                                                                                                                                                                                                            108
                                                                                                                                                        /organism-"Homo sapiens"
/db_xref="taxon:9606"
/clone="GLCGJG12"
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                         REFERENCE
                                AUTHORS
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Sequence 3, Appli Sequence 1, Appli Sequence 11, Appli Sequence 11, Appli Sequence 20, Appli Sequence 22, Appli Sequence 23, Appli Sequence 24, Appli Sequence 24, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 45, Appli

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GENERAL INFORMATION:
APPLICANT: GUENGERICH, F. Peter
APPLICANT: GUENGERICH, P. J.
APPLICANT: GUENGERICH, P. J.
TITLE OF INVENTION: EXPRESSION AND PURIFICATION OF
TITLE OF INVENTION: CYTOCHROME P450
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/194,981E
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Pred. No. 1.4e-42;
US-08-750-703-3

US-08-750-703-4

US-08-750-703-1

US-08-750-703-1

US-08-116-459-11

US-08-145-658D-20

US-08-145-658D-22

US-08-145-658D-22

US-08-145-658D-22

US-08-145-658D-21

US-08-145-658D-21

US-08-145-658D-21

US-08-145-658D-24

US-08-143-445-45

US-08-143-445-45

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Suite 1200, 127 Peachtree Street,
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REGISTPATION NUMBER: 38,298
REFERCE/DOCKET NUMBER: 22000.0022
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 688-0770
TELEFAX: (404) 688-0880
INFORMATION FOR SEQ ID NO: 4:
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BEDJUM TYPE: Floppy disk
CCMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                          GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-08-201-118-14
US-08-201-118-14
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Maximum DB seq
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                                                                                                                                                                                                                                                                                  Perfect score:
                                                                                                                                                                                                                                                                                                                                                       Scoring table:
                                                                                                                        OM nucleic
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                                                                                                                                                                                                                                                                                                             Seguence:
                                                                                                                                                                                                                                                                                                                                                                                                                              Searched:
                                                                                                                                                                 Run on:
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Length 1419;

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Sequence 10, Application US/08201118
Patent No. 5786191
GENERAL INFORMATION:
APPLICANT: GOLDSTEIN, Joyce A.
APPLICANT: RONKES-SPARKS, Marjoriè
TITLE OF INVENTION: CLONING AND EXPRESSION OF COMPLEMENTARY
TITLE OF INVENTION: SUBFAMILY
NUMBER OF SEQUENCES: 44
CORRESSORDING EACH AND EXPRESSION OF COMPLEMENTARY
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
     125 cctagctctcaaaggtctatggccctgtgttcactctgtattttggcctgaaacccatag 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                           245 ctggaagaggcatttcccactggctgaaagagctaacagaggatttggta 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          254 CIGGAAGAGGCATTITCCCACTGGCTGAAAGAGCTAACAGAGGATTTGGAA 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1852;
                                       245 ctggaagaggcattttcccactggctgaaagagctaacagaggatttggta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 163; DB 1; I
Pred. No. 1.6e-42;
0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Liebeschuetz, Joe
REGISTRATION NUMBER: 37,505
REFERNCE/DOCKET NUMBER: 15280-192-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/201,118 FILING DATE: 22-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/864,962
FILING DATE: 09-APR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                       STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21.9%;
97.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGIH: 1852 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         single
                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
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Best Local Similarity
Matches 166; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
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US-08-238-821B-10
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                                                                                                                                           US-08-201-118-10
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                                                                    Db
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                                 126 cctagctctcaaaggtctatggcctgtgttcactctgtattttggcctgaaacccatag 185
                                                                 110 CCAATCTCTCAAAGGTCTATGGCCCTGTGTTCACTCTGTATTTTGGCCTGAAACCCATAG 169
                                                                                                  Gaps
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                                                                                                                                                                       Length 1591;
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Pred. No. 1.5e-42;
 Indels
                                                                                                                                                                                                                                                                                                                                            APPLICANT: GUENGERICH, F. Peter
APPLICANT: GUO, Zuyu
APPLICANT: SANDHU, Punanh
APPLICANT: SANDHU, Punanh
APPLICANT: SANDHU, Punanh
APPLICANT: GUILLAN, Elizabeth M. J.
TITLE OF INVENTION: EXPRESSION AND PURIFICATION OF
TITLE OF INVENTION: CYTOCHROME P450
NUMBER OF SEQUENCES: 68
CORRESSONDENCE ADDRESS:
ADDRESSEE: NEEDLE 6 ROSENBERG, P.C.
STREET: Suite 1200, 127 Peachtree Street, NE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERAINE SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/194,981E
FILING DATE: February 10, 1994
CLASSIFICATION: 435
5,
Mismatches
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Patent No. 5886157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth Selby
REGISTRATION NUMBER: 38,298
REFERENCE/DOCKET NUMBER: 22000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 688-9880
INFORMATION FOR SED ID NO: 3:
SEQUENCE CHARACTERISTICS:
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COUNTR: USA
ZIP: 30303-1811
COMPUTER READABLE FORM:
TYPE: Floppy disk
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97.18;
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nucleic acid
EDNESS: single
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Best Local Similarity 97.13
Matches 166; Conservative
Conservative
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STATE: Georgia
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TOPOLOGY: lir
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US-08-194-981E-3
Matches 166;
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Townsend and Townsend Khourie and Crew

PC-DOS/MS-DOS

Floppy disk

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Sequence 10, Application PC/TUS9505744
GENERAL INFORMATION:
APPLICANT: GOLDSTEIN, JOyce A.
APPLICANT: GOLDSTEIN, Joyce A.
APPLICANT: DE MORIS, Sonia M.F.
ITILE OF INVENTION: CLOUNING, EXPRESSION AND DIAGNOSIS OF HUMAN
ITILE OF INVENTION: CYTOCHROME P450 2C19: THE PRINCIPAL DETERMINANT
ITILE OF INVENTION: OF S-MEPHYNYTOIN METABOLISM
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: PCI/US95/05744 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 29,684
REFERENCE/DOCKET NUMBER: 15280-192-1-1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION WIDMBER:
ILING DATE:
06-MAY-1994
PRIOR APPLICATION WIDMBER:
FILING DATE:
APPLICATION WIDMBER:
FILING DATE:
22-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION WIDMBER:
ILING DATE:
09-APR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                               ADDRESSEE: Townsend and Town
STREET: 379 Lytton Avenue
STATE: Palo Alto
STATE: California
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2402
INFORMATION FOR SEQ 1D NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1852 base pairs
                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dow, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
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       PCT-US95-05744-10
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Sequence 10, Application US/08238821B
Patent No. 5912120
GENERAL INFORMATION:
APPLICANT: GOLDSTEIN, Joyce A.
APPLICANT: DE MORES-SPARKS, Marjorie
APPLICANT: DE MORES-SPARKS, Marjorie
APPLICANT: DE MORES, Sonia M.F.
TITLE OF INVENTION: CYTOCHROME P450 2C19: THE PRINCIPAL DETERMINANT OF S-
TITLE OF INVENTION: MEPHENYTOIN METABOLISM
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ċ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21.9%; Score 163; DB 2; Length 1852:
ilarity 97.1%; Pred. No. 1.6e-42;
Conservative 0; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/238,821B
FILLING DATE: 06-MAY-1994
                                                                                                                                                                                                                                                    ADDRESSEE: Townsend and Townsend and Crew LLP STREEF: Two Pinbarcadero Center, 8th Floor CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15280-192110US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRICE APPLICATION DATA:
A.T.LICATION NUMBER: US 08/201,118
FILING DATE: 22-FEB-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION WUMBER: US 07/864,962
FILING DATE: 09-APR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Liebeschuetz, Joe
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 15,
TELECOMMUNICATION:
TELEPHONE: (650) 326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (650) 326-2422
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 1852 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 1.10
OTHER INFORMATION:
OTHER INFORMATION:
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Best Local Similarity
Matches 166; Conserv
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                                                                                                                                                                                                                                                                                                                                                                   94111
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                                                                                                                                                                    Gaps
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0
                                                                                                                                                                                                                                                                                                                                                    Length 1852;
                                                                                                                             Ouery Match 21.9%; Score 163; DB 5; Length 18 Best Local Similarity 97.1%; Pred. No. 1.6e-42; Matches 166; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/08201118
Patent No. 5786191
TYPE: nucleic acid
STRANDEDNESS: single
                                                    ; MOLECULE TYPE: CDNA PCI-US95-05744-10
                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 6
US-08-201-118-4
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RESULT

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(650) 326-2400
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SEQUENCE CHARACTERISTICS:
LENGTH: 1854 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS
                                                                                        2IP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: 1..12
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: Region
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es 156; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COPOLOGY:
                                    CITY: Sar
STATE: Ca
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-238-821B-4
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                APPLICANT: GOLDSTEIN, JOYCE A. APPLICANT: GOLDSTEIN, JOYCE A. APPLICANT: ROWRES-SPARKS, MAIJOIDE APPLICANT: ROWRES-SPARKS, MAIJOIDE TITLE OF INVENTION: CLOMING AND EXPRESSION OF COMPLEMENTARY TITLE OF INVENTION: SUBFAMILY SUBFAMILY SUBFAMILY CORRESPONDENCES: 44 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
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Patent No. 5912120
RENERAL INFORMATION:
APPLICANT: GOLDSTEIN, Joyce A.
APPLICANT: COLOSTEIN, Joyce A.
APPLICANT: DE MORAIS, Sonia M.F.
ITLE OF INVENTION: CYTOCHROME P450 2C19: THE PRINCIPAL SETERMINANT OF STILLE OF INVENTION: MEPHENYTOIN METABOLISM
ITLE OF SEQUENCES: 4.
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             126 cctagototoaaaggtotatggcootgtgttcactotgtattttggcotgaaacccatag 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         176 CCAATCTCTCAAAGGTCTATGGCCCTGTGTTTCACTCTGTATTTTGGCCTGAAACCCAAG 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21.9%; Score 163; DB 1; Length 1854; 97.1%; Pred. No. 1.6e-42;
                                                                                                                                        ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: 379 Lytton Avenue CITY: Palo Alto STATE: California
                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15280-192-1
                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/864,962
FILING DATE: 09-ARR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/201,118
FILING DATE: 22-FEB-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY AGENT INFORMATION.
NAME: Liebeschuetz, Joe
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 37,505
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (415) 326-2420
INFORMATION FOR SED ID NO: 4:
SEDUENCE CHARACTERISTICS:
LENGTH: 1854 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 21.99
Best Local Similarity 97.19
Matches 166; Conservative
                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
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US-08-201-118-4
GENERAL INFORMATION:
APPLICANT: GOLDS1
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Sequence 4, Application PC/TUS9505744

Sequence 4, Application PC/TUS9505744

GENERAL INFORMATION:
APPLICANT: GOLDSTEIN, Joyce A.
APPLICANT: ROMEES-SPARKS, Mariorie
APPLICANT: DE MORAIS, SONDIA M.F.
IIILE OF INVENTION: CLONING, EXPRESSION AND DIAGNOSIS OF HUMAN
IIILE OF INVENTION: CYTOCHROME P450 2019: THE PRINCIPAL DETERMINANT
IIILE OF INVENTION: OF S-MEPHYNYTOIN METABOLISM

NUMBER OF SEQUENCES: 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Corresponds to positions -12 to-1 for 25 of Figure 2."
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                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/238,821B
FILING DATE: OG-MAY-1994
CLASSIFICATION: 435
ADDRESSEE: Townsend and Townsend and Crew
STREET: Two Embarcadero Center, 8th Floor
CIIY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 15280-192110US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/864,962
FILING DATE: 09-APR-1992
AITONEY/AGENI INFORMATION:
NAME: Liebeschuetz, Joe
REGISTRATION NUMBER: 37,505
                                                                                                                                                                                                                                                                                                       FILING DATE: 06-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/201,118
FILING DATE: 22-FEB-1994
CLASSIFICATION: 435
                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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GENERAL INCORMATION:
GENERAL INCORMATION:
GENERAL INCORMATION:
APPLICANT: GOLDSTEIN, Joyce A.
APPLICANT: ROWKES-SPARKS, Marjorie
APPLICANT: DE MORAIS, Sonia M.F.
IIILE OF INVENTION: CLONING, EXPRESSION AND DIAGNOSIS OF HUMAN
TITLE OF INVENTION: CYTOCHROME P450 2c19: THE PRINCIPAL DETERMINANT OF S-
IIILE OF INVENTION: MEPHENYTOIN METABOLISM
NUMBER OF SEQUENCES: 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     126 cctageteteaaaggtetatggeeetgtgtteaetetgtattttggeetgaaaeeeatag 185
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                                                                                             COMPUTER: 18M PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/201,118
FILING DATE: 22-FEB-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/864,962
FILING DATE: 09-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Liebeschuetz, Joe
REGISTRATION NUMBER: 37,505
REGISTRATION NUMBER: 37,505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20.6%; Score 153.4; DB 1; 91.8%; Pred. No. 2e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITE. San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : Sequence 14, Application US/08238821B : Patent No. 5912120
                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 15
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFEMATION FOR SED ID NO: 14
SEQUENCE CHARACIERISTICS:
                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGIH: 1892 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 157; Conservative
    California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE IYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL:
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                                          94301
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                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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APPLICANT: GOLDSTEIN Joyce A.

APPLICANT: GOLDSTEIN Joyce A.

APPLICANT: GOLDSTEIN JOYCE A.

APPLICANT: GONES-SPARKS, Marjorie

TITLE OF INVENTION: CLONING AND EXPRESSION OF COMPLEMENTARY

TITLE OF INVENTION: SUBFAMILY

NUMBER OF SEQUENCES: 44

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend Khourie and Crew

STREET: 379 Lytton Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21.9%; Score 163; DB 5; Length 1854; ilarity 97.1%; Pred. No. 1.6e-42; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               246 ctggaagaggcattttcccactggctgaaagagctaacagaggatttggta 295
  Townsend and Townsend Khourie and Crew
                                                                                                                                                                                                      PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Dow, Raren B.
REGISTRATION UNDBER: 29,684
REFERENCE/DOCKET NUMBER: 15280-192-1-1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR PAPLICATION DATA:
APPLICATION NUMBER: US 08/238,821
FILING DATE: 06-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/201,118
FILING DATE: 22-FEB-1994
PRIOR APPLICATION NUMBER: US 07/864,962
FILING DATE: 09-APR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCI/US95/05744
                                                                                                                                                           IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 14, Application US/08201118 Patent No. 5786191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 4:
                   379 Lytton Avenue
                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 1854 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
      MOLECULE TYPE: CDNA
                                                                                                                                                                                OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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Best Local Similarity
Matches 166; Conserv
                                                                                                                                                                                                                                                                 FILING DATE
ALTARESSEE:
                                                                                                                                                                                                      SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                             COMPUTER:
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                                                                   FILING DATE:
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                SOFTWARE:
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GENERAL INFORMATION:
APPLICANT: GOLDSTEIN, JOyce A.
APPLICANT: ROMES-SPARKS, Marjorie
APPLICANT: BOMES-SPARKS, Marjorie
APPLICANT: DE MORAIS, Sonia M.F.
TITLE OF INVENTION: CLONING, EXPRESSION AND DIAGNOSIS OF HUMAN
TITLE OF INVENTION: CYTOCHROME P450 2C19: THE PRINCIPAL DETERMINANT
TITLE OF INVENTION: OF S-MEPHYNYTOIN METABOLISM
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Corresponds to positions -41 to-1 for 2c of Figure 2."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1892;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20.6%; Score 153.4; DB 2; 91.8%; Pred. No. 2e-39;
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                15280-192110US
                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/201,118
FILING DATE: 22-FEB-1994
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/864,962
FILING DATE: 09-APPL199
ATTORNEY/AGENT INFORMATION:
NAME: Liebeschuetz, Joe
REGISTRATION NUMBER: 37,528
REFERENCE/DOCKET NUMBER: 15280-19211
TELECOMMUNICATION:
              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/238,821B
FILING DATE: 06-MAY-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM IYPE: Floppy'disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                TELEPHONE: (650) 326-2400
TELEFAX: (650) 326-2422
INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  379 Lytton Avenue
                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1892 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 20.69

Best Local Similarity 91.89

Matches 157; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COTHER INFORMATION: f. (1)

COTHER INFORMATION: f. (1)

COTHER INFORMATION: f. (1)
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E: California
                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: Region
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PCT-US95-05744-14
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: GOLDSTEIN, Joyce A.
APPLICANT: ROWES-SPARKS, MATJORIE
IIILE OF INVENTION: CLOMING AND EXPRESSION OF COMPLEMENTARY
IIILE OF INVENTION: SUBFAMILY
NUMBER OF INVENTION: SUBFAMILY
CORRESPONDENCE: 44
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Townsend and Townsend Khourie and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM IYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERAING SYSEM: PC-DOS/MS-DOS
SOFIWARE: Patentin Release #1.0, Version #1.25
Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 153.4; DB 5;
Pred. No. 2e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 15280-192-1-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ 1D NO: 14:
SEQUENCE**CHARACTERISTICS:
                                                                           CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/238,821
FILING DATE: 06-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/201,118
FILING DATE: 22-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/864,962
FILING DATE: 09-APR-1992
ATTORNEY/AGEN INFORMATION:
NAME: DOW, KAIEN B.
REGISTATION NUMBER: 29,684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-201-118-2
; Sequence 2, Application US/08201118
; Patent No. 5786191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 379 Lytton Avenue CITY: Palo Alto STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 1892 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 20.6
Best Local Similarity 91.8
Matches 157; Conservative
                CURRENT APPLICATION DATA: APPLICATION NUMBER: PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM IYPE: Floppy
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SIRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: Region
LOCATION: 1..5
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                   TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-238-821B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 14
PCT-US95-05744-2
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APPLICANT: BOMKES-SPARKS, Marjorie
APPLICANT: DE MORAIS, Sonia M.F.
TITLE OF INVENTION: CLONING, EXPRESSION AND DIAGNOSIS OF HUMAN
TITLE OF INVENTION: CYTOCHROME P450 2C19: THE PRINCIPAL DETERMINANT OF S-
TITLE OF INVENTION: MEPHENYTOIN METABOLISM
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  333 ITTGGAAICGITITCAGCAAIGGAAAGAGAIGGAAGGAGAICCGGCGITICICCCICAIG 392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1745;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: PAPLICATION NUMBER: US/08/238,821B FILING DATE: U6-MAY-1994 CLASSIFICATION: 435 PRIOR APPLICATION DATA: PAPLICATION NUMBER: US 08/201,118 FILING DATE: 22-FEB1994 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20.1%; Score 149.6; DB 1
97.4%; Pred. No. 3.2e-38;
tive 0; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          453 CGCTGCCTTGTGGAGGAGTTGAGAAAACCAAGGCT 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     581 cgctgccttgtggaggagttgagaaaaaccaagggt 616
          CURRENT PELLCATION DATA

PULING DATE: 22-FEB-1994

FILING DATE: 22-FEB-1994

FILING DATE: 22-FEB-1994

FILING DATE: 20-FEB-1994

PROR APPLICATION DATA:

APPLICATION NUMBER: US 07/864,962

FILING DATE: 09-APR-1992

ATTONNEY, AGENT INFORMATION:

NAME: Liebeschuetz, Joe

REGISTRATION NUMBER: 37,505

REFERENCE/POCKET NUMBER: 15280-192-1

TELECHONE: (415) 326-2400

TELECHONE: (415) 326-2402

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACIERISTICS:

LENGTH: 1746 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08238821B
Patent No. 5912120
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: GOLDSTEIN, Joyce A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 20.18
Best Local Similarity 97.48
Matches 152; Conservative
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE:
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US-08-238-821B-2
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Sequence 2, Application PC/TUS9505744
GENERAL INFORMATION:
APPLICANT: GOLDSTEIN, JOYCE A.
APPLICANT: ROWEES-SPARKS, MATIOTIE
APPLICANT: DE MORAIS, Sonia M.F.
TITLE OF INVENTION: CLONING, EARRESSION AND DIAGNOSIS OF HUMAN
TITLE OF INVENTION: CYTOCHROME P450 2C19: THE PRINCIPAL DETERMINANT
TITLE OF INVENTION: OF S-MEPHYNYTOIN METABOLISM
NUMBER OF SEQUENCES:
ADDRESSEE: Townsend and Townsend Khourie and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Corresponds to positions -5 to-1 for 11a of Figure 2."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 20.1%; Score 149.6; DB 2; Length 1746; Best Local Similarity 97.4%; Pred. No. 3.2e-38; Matches 152; Conservative 0; Mismatches 4; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: 379 Lytton Avenue CITY: Palo Alto STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPITWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCI/US95/05744
                                                                                         NAME: Liebeschuetz, Joe

REGISTRATION NUMBER: 37,505

REFERNEC/COKET NUMBER: 15280-192110US

TELEPHONE: (650) 326-2400

TELEPHONE: (650) 326-242

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 1746 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            581 cgctgccttgtggaggagttgagaaaaaccaagggt 616
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APPLICATION NUMBER: US 07/864,962
FILING DATE: 09-APR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/238,821
FILING DATE: 06-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                393 ACGCTGCGGAAITTTGGGATGGGGAAGAGGGGCATTGAGGACCGTGTTCAAGAGGAAGCC 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 13 Application US/08716459

Sequence 13 Application US/08716459

Fatent No. 5821062.

GENERAL INFORMATI NO.

APPLICANT: KANEKO, Hideo

APPLICANT: KANEKO, Hideo

TILLE OF INVENTION: OLICONUCLEOTIDE FOR USE IN CHECKING

TITLE OF INVENTION: HUMAN-DERIVED CYTOCHROME P45011C13 GENE

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP

STREET P.O. Box 747

CITY: Falls Church

STATE: Virginia

CANTARINE OF SEQUENCES: 10 STATE: P.O. Box 747

CITY: Falls Church
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1745;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20.1%; Score 149.6; DB 5 97.4%; Pred. No. 3.2e-38; Live 0; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        581 cgctgccttgtggaggagttgagaaaaaccaagggt 616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: 1BM DOS Version 5.00 SOFTWARE: Word Perfect 5.1 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/716.459 FILING DATE: 27 SEPIEMBER 1996 CLASSIFICATION: 536
                                                                                                                               NAME: Dow, Karen B.
REGISTRATION NUMBER: 29,684
REFERENCE/DOCKET NUMBER: 15280-192-1-1
TELECHUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP-059385/1994
APPLICATION NUMBER: JP-059386/1994
FILING DATE: 29-03-1994
FILING DATE: 29-03-1994
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: US 08/201,118
FILING DATE: 22-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/864,962
FILING DATE: 09-ARR-1992
ATT.JANEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                           LENGTH: 1746 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLXX: linear
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 97.4
Matches 152; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IBM PC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
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Gaps
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                                                                                                                                                                                   DNA fragment obtained by
                                                                                                                                                                                                                                                      Score 144; DB 1; Length 200;
Pred. No. 5.8e-37;
0; Mismatches 20; Indels
                     REFERENCE/DOCKET NUMBER: 20-4081PCT TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: April 19, 2002, 08:10:39
Job time: 2939 sec
                                                                                                                                                                     : TOPOLOGY: linear

: MOLECULE TYPE: Other nucleic acid

: MOLECULE TYPE: cloning

US-08-716-459-13
ard R.
30,330
                                                  TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
TELEX: 248345
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 88.6%;
Matches 156; Conservative
SVENSSON, Leonard
                                                                                                                        LENGTH: 200
TYPE: nucleic acid
STRANDEDNESS: single
          REGISTRATION NUMBER:
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